

SEQUENCE LISTING

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 White, David
 Pan, Yang

<120> NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
 STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 THEREFOR

<130> MNI-121CP

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<150> PCT/US00/02125

<151> 2000-01-27

<150> 09/448,076

<151> 1999-11-23

<150> 09/276,400

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<170> PatentIn Ver. 2.0

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Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile Leu Cys Ser Val
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Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile
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gcc acc aat gcc acc aga gtc atc cat gac aac tat gat cag ctg gag      486
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gtc cac gct gct gcc att aaa tcc ctg gga gag ctc gac gtc ttt cta      534
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Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
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Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
50 55 60
Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
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Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
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Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
100 105 110
Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
115 120 125
Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
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Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
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 gac atg cac cat ata gaa gag agt ttc caa gaa atc aaa aga gcc atc 144
 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
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 caa gct aag gac acc ttc cca aat gtc act atc ctg tcc aca ttg gag 192
 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
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 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
 65 70 75 80
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 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
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 aac ccc aaa atc ttg aga aaa atc agc agc att gcc aac tct ttc ctc 336
 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
 100 105 110
 tac atg cag aaa act ctg cgg caa tgt cag gaa cag agg cag tgt cac 384
 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
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 tgc agg cag gaa gcc acc aat gcc acc aga gtc atc cat gac aac tat 432
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 130 135 140
 gat cag ctg gag gtc cac gct gct gcc att aaa tcc ctg gga gag ctc 480
 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
 145 150 155 160
 gac gtc ttt cta gcc tgg att aat aag aat cat gaa gta atg tcc tca 528
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 gct 531
 Ala

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 35 40 45
 Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg
 50 55 60
 Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile
 65 70 75 80
 Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
 85 90 95
 Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn Ala
 100 105 110
 Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His Ala Ala
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 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
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 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
 65 70 75 80

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Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
100 105 110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Arg Cys His Arg
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Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
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Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
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35 40 45

Ser Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile
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Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro
85 90 95

Gln Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu
100 105 110

Gly Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg
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Phe Leu Lys Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser
130 135 140

Asp Phe Asn Lys Leu Glu Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
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Phe Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met
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Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Met
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Leu Leu Asp Gly Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
 65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
 85 90 95

Gln Ala Glu Asn His Ser Thr Asp Gln Glu Lys Asp Lys Val Asn Ser
 100 105 110

Leu Gly Glu Lys Leu Lys Thr Leu Arg Val Arg Leu Arg Arg Cys His
 115 120 125

Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys
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Met Lys Asn

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Ser Cys Gln Val Thr Gly Val Val Leu Pro Glu Leu Trp Glu Ala Phe
35 40 45
Trp Thr Val Lys Asn Thr Val Gln Thr Gln Asp Asp Ile Thr Ser Ile
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Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr Val Phe
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Lys Asn Tyr His Ser Lys Ile Ala Lys Phe Lys Val Leu Arg Ser Phe
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Ser Thr Leu Ala Asn Asn Phe Ile Val Ile Met Ser Gln Leu Gln Pro
115 120 125
Ser Lys Asp Asn Ser Met Leu Pro Ile Ser Glu Ser Ala His Gln Arg
130 135 140
Phe Leu Leu Phe Arg Arg Thr Phe Lys Gln Leu Asp Thr Glu Val Ala
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Gln Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
35 40 45
Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg Leu
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Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser Cys Tyr
65 70 75 80
Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn
85 90 95
Tyr His Asn Arg Thr Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr
100 105 110

Tyr Lys Leu

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Ala Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg
95 100 105

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Ile Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr	
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gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag	556
Glu Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu	
125 130 135	
gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac	604
Asp Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp	
140 145 150	
tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga	652
Ser Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg	
155 160 165 170	
att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag	700
Ile Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu	
175 180 185	
ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac	748
Gly Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp	
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Lys Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly	
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Phe Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala	
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Gln Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly	
235 240 245 250	
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Thr Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn	
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Asp Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val	
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Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln	
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cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca	1132
Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr	
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Val Cys Asp Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg	
335 340 345	

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gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac Asp Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr 395 400 405 410	1372
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Trp His Glu Cys His Gly His Tyr His Ser Met Asp Ile Phe Thr His	
605 610 615	
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Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys	
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Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr	
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Cys Lys Tyr Asp Gly His Arg Ile Trp Val His Asn Cys His Ile Gly	
715 720 725 730	
gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc	2380
Asp Ala Phe Ser Glu Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly	
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Gln Thr Ser Asn Gln Ile Ile	
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      50              55              60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
      65              70              75              80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
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Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
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Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
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Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
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Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
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Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
      245              250              255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
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305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val
420 425 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp
435 440 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu
450 455 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
465 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala
515 520 525

Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
530 535 540

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys
545 550 555 560

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
565 570 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe
580 585 590

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Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
 595 600 605
 His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro
 610 615 620
 Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu
 625 630 635 640
 Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn
 645 650 655
 Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His
 660 665 670
 Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
 675 680 685
 Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
 690 695 700
 Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
 705 710 715 720
 Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
 725 730 735
 Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile
 740 745 750

Ile

<210> 12
 <211> 2262
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2259)

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 Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
 1 5 10 15
 tgc ctg ctg tgc agt tcg tgc ttg ggg tct ccg tcc cct tcc acg ggc 96
 Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
 20 25 30
 cct gag aag aag gcc ggg agc cag ggg ctt cgg ttc cgg ctg gct ggc 144
 Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
 35 40 45
 ttc ccc agg aag ccc tac gag ggc cgc gtg gag ata cag cga gct ggt 192
 Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
 50 55 60

- 16 -

gaa tgg ggc acc atc tgc gat gat gac ttc acg ctg cag gct gcc cac	240
Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His	
65 70 75 80	
atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg acc cac	288
Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His	
85 90 95	
agt gcc aaa tat ggc cct gga aca ggc cgc atc tgg ctg gac aac ttg	336
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu	
100 105 110	
agc tgc agt ggg acc gag cag agt gtg act gaa tgt gcc tcc cgg ggc	384
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly	
115 120 125	
tgg ggg aac agt gac tgt acg cac gat gag gat gct ggg gtc atc tgc	432
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys	
130 135 140	
aaa gac cag cgc ctc cct ggc ttc tcg gac tcc aat gtc att gag gta	480
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val	
145 150 155 160	
gag cat cac ctg caa gtg gag gag gtg cga att cga ccc gcc gtt ggg	528
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly	
165 170 175	
tgg ggc aga cga ccc ctg ccc gtg acg gag ggg ctg gtg gaa gtc agg	576
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg	
180 185 190	
ctt cct gac ggc tgg tcg caa gtg tgc gac aaa ggc tgg agc gcc cac	624
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His	
195 200 205	
aac agc cac gtg gtc tgc ggg atg ctg ggc ttc ccc agc gaa aag agg	672
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg	
210 215 220	
gtc aac gcg gcc ttc tac agg ctg cta gcc caa cgg cag caa cac tcc	720
Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser	
225 230 235 240	
ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg gag gcc cac ctc tcc	768
Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser	
245 250 255	
ctc tgt tcc ctg gag ttc tat cgt gcc aat gac acc gcc agg tgc cct	816
Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro	
260 265 270	
ggg ggg ggc cct gca gtg gtg agc tgt gtg cca ggc cct gtc tac gcg	864
Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala	
275 280 285	
gca tcc agt ggc cag aag aag caa caa cag tcg aag cct cag ggg gag	912
Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu	
290 295 300	

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gcc cgt gtc cgt cta aag ggc ggc gcc cac cct gga gag ggc cgg gta	960
Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val	
305 310 315 320	
gaa gtc ctg aag gcc agc aca tgg ggc aca gtc tgt gac cgc aag tgg	1008
Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp	
325 330 335	
gac ctg cat gca gcc agc gtg gtg tgt cgg gag ctg ggc ttc ggg agt	1056
Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser	
340 345 350	
gct cga gaa gct ctg agt ggc gct cgc atg ggg cag ggc atg ggt gct	1104
Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala	
355 360 365	
atc cac ctg agt gaa gtt cgc tgc tct gga cag gag ctc tcc ctc tgg	1152
Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp	
370 375 380	
aag tgc ccc cac aag aac atc aca gct gag gat tgt tca cat agc cag	1200
Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln	
385 390 395 400	
gat gcc ggg gtc cgg tgc aac cta cct tac act ggg gca gag acc agg	1248
Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg	
405 410 415	
atc cga ctc agt ggg ggc cgc agc caa cat gag ggg cga gtc gag gtg	1296
Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val	
420 425 430	
caa ata ggg gga cct ggg ccc ctt cgc tgg ggc ctc atc tgt ggg gat	1344
Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp	
435 440 445	
gac tgg ggg acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg	1392
Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu	
450 455 460	
ggc tac gcc aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg	1440
Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly	
465 470 475 480	
aat ata aca gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag	1488
Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu	
485 490 495	
ctg tcc ctg gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag	1536
Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys	
500 505 510	
agg aca ggg acc cgc ttc act gct gga gtc atc tgt tct gag act gca	1584
Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala	
515 520 525	
tca gat ctg ttg ctg cac tca gca ctg gtg cag gag acc gcc tac atc	1632
Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile	
530 535 540	

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gaa gac cgg ccc ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc	1680
Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys	
545 550 555 560	
ctg gcc agc tca gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt	1728
Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg	
565 570 575	
ctg ctc cga ttc tcc tcc cag atc cac aac ctg gga cga gct gac ttc	1776
Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe	
580 585 590	
agg ccc aag gct ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg	1824
Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly	
595 600 605	
cat tac cac agc atg gac atc ttc act cac tat gat atc ctc acc cca	1872
His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro	
610 615 620	
aat ggc acc aag gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa	1920
Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu	
625 630 635 640	
gac act gag tgt cag gag gat gtc tcc aag cgg tat gag tgt gcc aac	1968
Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn	
645 650 655	
ttt gga gag caa ggc atc act gtg ggt tgc tgg gat ctc tac cgg cat	2016
Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His	
660 665 670	
gac att gac tgt cag tgg att gac atc acg gat gtg aag cca gga aac	2064
Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn	
675 680 685	
tac att ctc cag gtt gtc atc aac cca aac ttt gaa gta gca gag agt	2112
Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser	
690 695 700	
gac ttt acc aac aat gca atg aaa tgt aac tgc aaa tat gat gga cat	2160
Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His	
705 710 715 720	
aga atc tgg gtg cac aac tgc cac att ggt gat gcc ttc agt gaa gag	2208
Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu	
725 730 735	
gcc aac agg agg ttt gaa cgc tac cct ggc cag acc agc aac cag att	2256
Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile	
740 745 750	
atc taa	2262
Ile	
<210> 13	
<211> 38	
<212> PRT	
<213> Artificial Sequence	

<220>

<223> Description of Artificial Sequence: (SRRD)
consensus sequence

<220>

<223> Any occurrences of Xaa may be any amino acid

<400> 13

Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa
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Trp Gly Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Cys Xaa Xaa Xaa Gly
35

<210> 14

<211> 417

<212> PRT

<213> Homo sapiens

<400> 14

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1 5 10 15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
20 25 30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
35 40 45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
50 55 60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
65 70 75 80

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
85 90 95

Asn Arg Thr Ala Ala Gly Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
100 105 110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
115 120 125

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Pro Ser Arg Ala Glu Asn
130 135 140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
145 150 155 160

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
165 170 175

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Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
180 185 190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
195 200 205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
210 215 220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
225 230 235 240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
245 250 255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
260 265 270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
275 280 285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
290 295 300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
305 310 315 320

Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
325 330 335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
340 345 350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
355 360 365

Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
405 410 415

Tyr

<210> 15

<211> 574

<212> PRT

<213> Homo sapiens

<400> 15

Met Ala Leu Ala Arg Gly Ser Arg Gln Leu Gly Ala Leu Val Trp Gly
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Ala Cys Leu Cys Val Leu Val His Gly Gln Gln Ala Gln Pro Gly Gln
20 25 30

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Gly Ser Asp Pro Ala Arg Trp Arg Gln Leu Ile Gln Trp Glu Asn Asn
 35 40 45

Gly Gln Val Tyr Ser Leu Leu Asn Ser Gly Ser Glu Tyr Val Pro Ala
 50 55 60

Gly Pro Gln Arg Ser Glu Ser Ser Ser Arg Val Leu Leu Ala Gly Ala
 65 70 75 80

Pro Gln Ala Gln Gln Arg Arg Ser His Gly Ser Pro Arg Arg Arg Gln
 85 90 95

Ala Pro Ser Leu Pro Leu Pro Gly Arg Val Gly Ser Asp Thr Val Arg
 100 105 110

Gly Gln Ala Arg His Pro Phe Gly Phe Gly Gln Val Pro Asp Asn Trp
 115 120 125

Arg Glu Val Ala Val Gly Asp Ser Thr Gly Met Ala Leu Ala Arg Thr
 130 135 140

Ser Val Ser Gln Gln Arg His Gly Gly Ser Ala Ser Ser Val Ser Ala
 145 150 155 160

Ser Ala Phe Ala Ser Thr Tyr Arg Gln Gln Pro Ser Tyr Pro Gln Gln
 165 170 175

Phe Pro Tyr Pro Gln Ala Pro Phe Val Ser Gln Tyr Glu Asn Tyr Asp
 180 185 190

Pro Ala Ser Arg Thr Tyr Asp Gln Gly Phe Val Tyr Tyr Arg Pro Ala
 195 200 205

Gly Gly Gly Val Gly Ala Gly Ala Ala Ala Val Ala Ser Ala Gly Val
 210 215 220

Ile Tyr Pro Tyr Gln Pro Arg Ala Arg Tyr Glu Glu Tyr Gly Gly Gly
 225 230 235 240

Glu Glu Leu Pro Glu Tyr Pro Pro Gln Gly Phe Tyr Pro Ala Pro Glu
 245 250 255

Arg Pro Tyr Val Pro Pro Pro Pro Pro Pro Pro Asp Gly Leu Asp Arg
 260 265 270

Arg Tyr Ser His Ser Leu Tyr Ser Glu Gly Thr Pro Gly Phe Glu Gln
 275 280 285

Ala Tyr Pro Asp Pro Gly Pro Glu Ala Ala Gln Ala His Gly Gly Asp
 290 295 300

Pro Arg Leu Gly Trp Tyr Pro Pro Tyr Ala Asn Pro Pro Pro Glu Ala
 305 310 315 320

Tyr Gly Pro Pro Arg Ala Leu Glu Pro Pro Tyr Leu Pro Val Arg Ser
 325 330 335

Ser Asp Thr Pro Pro Pro Gly Gly Glu Arg Asn Gly Ala Gln Gln Gly
 340 345 350

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Arg Leu Ser Val Gly Ser Val Tyr Arg Pro Asn Gln Asn Gly Arg Gly
 355 360 365

Leu Pro Asp Leu Val Pro Asp Pro Asn Tyr Val Gln Ala Ser Thr Tyr
 370 375 380

Val Gln Arg Ala His Leu Tyr Ser Leu Arg Cys Ala Ala Glu Glu Lys
 385 390 395 400

Cys Leu Ala Ser Thr Ala Tyr Ala Pro Glu Ala Thr Asp Tyr Asp Val
 405 410 415

Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ala
 420 425 430

Asp Phe Leu Pro Asn Arg Pro Arg His Thr Trp Glu Trp His Ser Cys
 435 440 445

His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu
 450 455 460

Asp Ala Ala Thr Gly Lys Lys Val Ala Glu Gly His Lys Ala Ser Phe
 465 470 475 480

Cys Leu Glu Asp Ser Thr Cys Asp Phe Gly Asn Leu Lys Arg Tyr Ala
 485 490 495

Cys Thr Ser His Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr
 500 505 510

Asn Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Gln Pro
 515 520 525

Gly Asn Tyr Ile Leu Lys Val His Val Asn Pro Lys Tyr Ile Val Leu
 530 535 540

Glu Ser Asp Phe Thr Asn Asn Val Val Arg Cys Asn Ile His Tyr Thr
 545 550 555 560

Gly Arg Tyr Val Ser Ala Thr Asn Cys Lys Ile Val Gln Ser
 565 570

<210> 16
 <211> 774
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
 1 5 10 15

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His
 20 25 30

Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln
 35 40 45

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Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys
 50 55 60
 Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp
 65 70 75 80
 Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val
 85 90 95
 Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser
 100 105 110
 Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys
 115 120 125
 Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly
 130 135 140
 Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp
 145 150 155 160
 Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile
 165 170 175
 Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu
 180 185 190
 Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val
 195 200 205
 Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala
 210 215 220
 Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg
 225 230 235 240
 Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln
 245 250 255
 Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile
 260 265 270
 Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn
 275 280 285
 Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly
 290 295 300
 Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys
 305 310 315 320
 Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu
 325 330 335
 Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp
 340 345 350
 Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly
 355 360 365

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Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly
 370 375 380
 Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys
 385 390 395 400
 Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His
 405 410 415
 Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln
 420 425 430
 Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val
 435 440 445
 Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys
 450 455 460
 Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu
 465 470 475 480
 Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His
 485 490 495
 Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser
 500 505 510
 Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val
 515 520 525
 Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser
 530 535 540
 Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr
 545 550 555 560
 Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu
 565 570 575
 Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly
 580 585 590
 Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln
 595 600 605
 Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp
 610 615 620
 Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu
 625 630 635 640
 Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
 645 650 655
 Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu
 660 665 670
 Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met
 675 680 685

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Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro
 690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val
 705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr
 725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe
 740 745 750

Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu Leu Asn
 755 760 765

Asn Gln Leu Ser Pro Gln
 770

<210> 17
 <211> 754
 <212> PRT
 <213> Mus musculus

<400> 17
 Met Arg Ala Val Ser Val Trp Tyr Cys Cys Pro Trp Gly Leu Leu Leu
 1 5 10 15

Leu His Cys Leu Cys Ser Phe Ser Val Gly Ser Pro Ser Pro Ser Ile
 20 25 30

Ser Pro Glu Lys Lys Val Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala
 35 40 45

Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala
 50 55 60

Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala
 65 70 75 80

His Val Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr
 85 90 95

His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn
 100 105 110

Leu Ser Cys Arg Gly Thr Glu Gly Ser Val Thr Glu Cys Ala Ser Arg
 115 120 125

Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile
 130 135 140

Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu
 145 150 155 160

Val Glu His Gln Leu Gln Val Glu Glu Val Arg Leu Arg Pro Ala Val
 165 170 175

Glu Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val
 180 185 190

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Arg Leu Pro Glu Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala
 195 200 205
 His Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Gly Glu Lys
 210 215 220
 Arg Val Asn Met Ala Phe Tyr Arg Met Leu Ala Gln Lys Lys Gln His
 225 230 235 240
 Ser Phe Gly Leu His Ser Val Ala Cys Val Gly Thr Glu Ala His Leu
 245 250 255
 Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Thr Arg Cys
 260 265 270
 Ser Gly Gly Asn Pro Ala Val Val Ser Cys Val Leu Gly Pro Leu Tyr
 275 280 285
 Ala Thr Phe Thr Gly Gln Lys Lys Gln Gln His Ser Lys Pro Gln Gly
 290 295 300
 Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His Gln Gly Glu Gly Arg
 305 310 315 320
 Val Glu Val Leu Lys Ala Gly Thr Trp Gly Thr Val Cys Asp Arg Lys
 325 330 335
 Trp Asp Leu Gln Ala Ala Ser Val Val Cys Pro Glu Leu Gly Phe Gly
 340 345 350
 Thr Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly
 355 360 365
 Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Pro Ser Leu
 370 375 380
 Trp Arg Cys Pro Ser Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser
 385 390 395 400
 Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Val Glu Thr
 405 410 415
 Lys Ile Arg Leu Ser Gly Gly Arg Ser Arg Tyr Glu Gly Arg Val Glu
 420 425 430
 Val Gln Ile Gly Ile Pro Gly His Leu Arg Trp Gly Leu Ile Cys Gly
 435 440 445
 Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly
 450 455 460
 Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser
 465 470 475 480
 Gly Asn Val Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Ser
 485 490 495
 Glu Leu Ser Leu Asn Gln Cys Ala His Ser Ser His Ile Thr Cys
 500 505 510

1

10

10

- 28 -

<400> 18

Trp Glu Trp His Ser Cys His Gln His Tyr His
 1 5 10

<210> 19

<211> 451

<212> PRT

<213> Homo sapiens

<400> 19

Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser
 1 5 10 15

Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu
 20 25 30

Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser
 35 40 45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu
 50 55 60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
 65 70 75 80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser
 85 90 95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu
 100 105 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile
 115 120 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe
 130 135 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser
 145 150 155 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile
 165 170 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu
 180 185 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln
 195 200 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala
 210 215 220

Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile
 225 230 235 240

Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu
 245 250 255

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Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln
 260 265 270

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly
 275 280 285

Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu
 290 295 300

Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro
 305 310 315 320

Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly
 325 330 335

Glu Lys Gly Ser Gly Asn Thr Leu Thr Pro Phe Thr Lys Val Arg Leu
 340 345 350

Val Gly Gly Ser Gly Pro His Glu Gly Arg Val Glu Ile Leu His Ser
 355 360 365

Gly Gln Trp Gly Thr Ile Cys Asp Asp Arg Trp Glu Val Arg Val Gly
 370 375 380

Gln Val Val Cys Arg Ser Leu Gly Tyr Pro Gly Val Gln Ala Val His
 385 390 395 400

Lys Ala Ala His Phe Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu
 405 410 415

Val Phe Cys Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg
 420 425 430

Gln Trp Gly Thr Arg Ala Cys Ser His Ser Glu Asp Ala Gly Val Thr
 435 440 445

Cys Thr Leu
 450

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 gcttaccaag aaacccatgt cagc

24

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

- 30 -

<400> 21
ggcagttagt caggtgctgc

20

<210> 22
<211> 981
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (107)..(748)

<400> 22
gaattcgggca cgaggggccg caccgccg ccacccagc ctcaaactgc agtccggcgc 60
cgcggggag gacaagggga aggaataaac acgtttggtg agagcc atg gca ctc 115
Met Ala Leu
1
aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc 163
Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe
5 10 15
cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg 211
Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg
20 25 30 35
cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag 259
Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln
40 45 50
tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg 307
Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly
55 60 65
gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac 355
Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp
70 75 80
tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac 403
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn
85 90 95
cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg 451
Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly
100 105 110 115
gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa 499
Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln
120 125 130
gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca 547
Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro
135 140 145
cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc acc gtc tcc 595
His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser Thr Val Ser
150 155 160

- 31 -

agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt gct ctg gcc 643
 Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala
 165 170 175

acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac tgc aag agg 691
 Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg
 180 185 190 195

cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc ctc tgt ctc 739
 Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser Leu Cys Leu
 200 205 210

act gtg aag tgagcttggt agcattgtca cccaagagtt ctcaagacac 788
 Thr Val Lys

ctggctgaga cctaagacct ttagagcatc aacagctact tagaatacaa gatgcaggaa 848

aacgagcctc ttcaggaatc tcagggcctc ctagggatgc tggcaaggct gtgatgtctc 908

aaggctacca ggaaaaaata aaagttgtct ataccctaaa aaaaaaaaaa aaaaaaaaaa 968

aacatgcggc cgc 981

<210> 23
 <211> 214
 <212> PRT
 <213> Mus musculus

<400> 23
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140

Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
 145 150 155 160

- 32 -

Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 165 170 175

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
 180 185 190

Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser
 195 200 205

Leu Cys Leu Thr Val Lys
 210

<210> 24
 <211> 642
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(642)

<400> 24
 atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc 48
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15

att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga 96
 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30

gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc 144
 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45

tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc 192
 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60

ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc 240
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80

aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg 288
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95

ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct 336
 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110

gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt 384
 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125

ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc 432
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140

- 33 -

tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc 480
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
145 150 155 160

acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt 528
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
165 170 175

gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac 576
Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
180 185 190

tgc aag agg cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc 624
Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser
195 200 205

ctc tgt ctc act gtg aag 642
Leu Cys Leu Thr Val Lys
210

<210> 25

<211> 555

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(555)

<400> 25

gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac 48
Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn
1 5 10 15

tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa 96
Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu
20 25 30

tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg 144
Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro
35 40 45

cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg 192
His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala
50 55 60

gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc 240
Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr
65 70 75 80

agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc 288
Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr
85 90 95

aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca 336
Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro
100 105 110

tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac 406
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn

85 90 95

- 35 -

cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg 454
Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly
100 105 110 115

gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa 502
Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln
120 125 130

gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca 550
Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro
135 140 145

cac tgt gag tgatgtgccca agtggcagca gaccttttaa aaaaaaagaa 599
His Cys Glu
150

aaaaaaacaa acaaaaacaa aaaaaaaaaa aaaaaaaaaa aaattttccgc ggccgc 655

<210> 27
<211> 150
<212> PRT
<213> Mus musculus

<400> 27
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
20 25 30

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
35 40 45

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
50 55 60

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
65 70 75 80

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
85 90 95

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
100 105 110

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
115 120 125

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
130 135 140

Tyr Glu Pro His Cys Glu
145 150

- 36 -

<210> 28
 <211> 450
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(450)

<400> 28
 atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc 48
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15
 att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga 96
 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30
 gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc 144
 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45
 tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc 192
 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60
 ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc 240
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80
 aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg 288
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95
 ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct 336
 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110
 gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt 384
 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125
 ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc 432
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140
 tac gaa cca cac tgt gag 450
 Tyr Glu Pro His Cys Glu
 145 150

<210> 29
 <211> 363
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(363)

- 37 -

<400> 29

gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac 48
 Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn
 1 5 10 15

tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa 96
 Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu
 20 25 30

tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg 144
 Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro
 35 40 45

cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg 192
 His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala
 50 55 60

gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc 240
 Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr
 65 70 75 80

agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc 288
 Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr
 85 90 95

aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca 336
 Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro
 100 105 110

cct cct ccc tac gaa cca cac tgt gag 363
 Pro Pro Pro Tyr Glu Pro His Cys Glu
 115 120

<210> 30

<211> 272

<212> PRT

<213> Mus musculus

<400> 30

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Leu Leu Leu Leu Ala Leu
 1 5 10 15

Thr Leu Gly Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr
 20 25 30

Pro Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met
 35 40 45

Val Ser Arg Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu
 50 55 60

Thr Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys
 65 70 75 80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr
 85 90 95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg
 100 105 110

- 38 -

Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro
 115 120 125
 Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn
 130 135 140
 Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu
 145 150 155 160
 Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu
 165 170 175
 Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val
 180 185 190
 Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro
 195 200 205
 Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu
 210 215 220
 Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp
 225 230 235 240
 Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr
 245 250 255
 Pro Ile Gln Glu Glu His Thr Asp Ala His Phe Thr Leu Ala Lys Ile
 260 265 270

<210> 31
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (273)..(1022)

<400> 31
 gaattcggaa cgaggggaac ctaattctcc tgaggctgag ggaggggtgga ggggtctcaag 60
 gcaacgctgg cccacgacg gactgccagg agcactaaca gtacccttag cttgctttcc 120
 tcctccctcc tttttatttt caagttcctt tttatttctc cttgcgtaac aaccttcttc 180
 ccttctgcac cactgcccgt acccttacct gccccgccac ctcttgcta cccactctt 240
 gaaaccacag ctgttggcag ggtccccagc tc atg cca gcc tca tct cct ttc 293
 Met Pro Ala Ser Ser Pro Phe
 1 5
 ttg cta gcc ccc aaa ggg cct cca ggc aac atg ggg ggc cca gtc aga 341
 Leu Leu Ala Pro Lys Gly Pro Pro Gly Asn Met Gly Gly Pro Val Arg
 10 15 20

gag ccg gca ctc tca gtt gcc ctc tgg ttg agt tgg ggg gca gct ctg 389
Glu Pro Ala Leu Ser Val Ala Leu Trp Leu Ser Trp Gly Ala Ala Leu
25 30 35

ggg gcc gtg gct tgt gcc atg gct ctg ctg acc caa caa aca gag ctg 437
Gly Ala Val Ala Cys Ala Met Ala Leu Leu Thr Gln Gln Thr Glu Leu
40 45 50 55

cag agc ctc agg aga gag gtg agc cgg ctg cag ggg aca gga ggc ccc 485
Gln Ser Leu Arg Arg Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro
60 65 70

tcc cag aat ggg gaa ggg tat ccc tgg cag agt ctc ccg gag cag agt 533
Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser
75 80 85

tcc gat gcc ctg gaa gcc tgg gag aat ggg gag aga tcc cgg aaa agg 581
Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg
90 95 100

aga gca gtg ctc acc caa aaa cag aag aag cag cac tct gtc ctg cac 629
Arg Ala Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His
105 110 115

ctg gtt ccc att aac gcc acc tcc aag gat gac tcc gat gtg aca gag 677
Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
120 125 130 135

gtg atg tgg caa cca gct ctt agg cgt ggg aga ggc cta cag gcc caa 725
Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln
140 145 150

gga tat ggt gtc cga atc cag gat gct gga gtt tat ctg ctg tat agc 773
Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser
155 160 165

cag gtc ctg ttt caa gac gtg act ttc acc atg ggt cag gtg gtg tct 821
Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln Val Val Ser
170 175 180

cga gaa ggc caa gga agg cag gag act cta ttc cga tgt ata aga agt 869
Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser
185 190 195

atg ccc tcc cac ccg gac cgg gcc tac aac agc tgc tat agc gca ggt 917
Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly
200 205 210 215

gtc ttc cat tta cac caa ggg gat att ctg agt gtc ata att ccc cgg 965
Val Phe His Leu His Gln Gly Asp Ile Leu Ser Val Ile Ile Pro Arg
220 225 230

gca agg gcg aaa ctt aac ctc tct cca cat gga acc ttc ctg ggg ttt 1013
Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly Thr Phe Leu Gly Phe
235 240 245

gtg aaa ctg tgattgtgtt ataaaaagtg gctcccagct tggaagacca 1062
Val Lys Leu
250

- 40 -

gggtgggtac atactggaga cagccaagag ctgagtatat aaaggagagg gaatgtgcag 1122
 gaacagagggc atcttcctgg gtttggctcc ccgttcctca cttttccctt ttcattccca 1182
 ccccttagac tttgatttta cggatatctt gcttctgttc cccatggagc tccgaattct 1242
 tgcgtgtgtg tagatgaggg gcgggggacg ggcgccaggc attgttcaga cctggtcggg 1302
 gcccactgga agcatccaga acagcaccac catctagcgg cc 1344

<210> 32
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1 5 10 15
 Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
 20 25 30
 Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
 35 40 45
 Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
 50 55 60
 Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp
 65 70 75 80
 Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
 85 90 95
 Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys
 100 105 110
 Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
 115 120 125
 Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
 130 135 140
 Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
 145 150 155 160
 Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
 165 170 175
 Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
 180 185 190
 Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
 195 200 205
 Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
 210 215 220

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Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
 225 230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
 245 250

<210> 33

<211> 754

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(750)

<400> 33

atg cca gcc tca tct cct ttc ttg cta gcc ccc aaa ggg cct cca ggc 48
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1 5 10 15

aac atg ggg ggc cca gtc aga gag ccg gca ctc tca gtt gcc ctc tgg 96
 Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
 20 25 30

ttg agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg 144
 Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
 35 40 45

ctg acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cgg 192
 Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
 50 55 60

ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg 240
 Leu Gln Gly Thr Gly Glu Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp
 65 70 75 80

cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat 288
 Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
 85 90 95

ggg gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag 336
 Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys
 100 105 110

aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag 384
 Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
 115 120 125

gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt 432
 Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
 130 135 140

ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct 480
 Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
 145 150 155 160

gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc 528
 Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
 165 170 175

- 42 -

acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act 576
Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
180 185 190

cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac 624
Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
195 200 205

aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att 672
Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
210 215 220

ctg agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca 720
Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
225 230 235 240

cat gga acc ttc ctg ggg ttt gtg aaa ctg tgat 754
His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 34
<211> 17
<212> PRT
<213> Homo sapiens

<400> 34
Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu
1 5 10 15

Phe

<210> 35
<211> 49
<212> PRT
<213> Homo sapiens

<400> 35
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
1 5 10 15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
20 25 30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
35 40 45

Leu

<210> 36
<211> 603
<212> DNA
<213> Homo sapiens

<222> (1) .. (603)

acc Thr 1	caa Gln	caa Gln	aca Thr	gag Glu 5	ctg Leu	cag Gln	agc Ser	ctc Leu	agg Arg 10	aga Arg	gag Glu	gtg Val	agc Ser	cgg Arg 15	ctg Leu	48
cag Gln	ggg Gly	aca Thr	gga Gly	ggc Gly	ccc Pro	tcc Ser	cag Gln	aat Asn	ggg Gly	gaa Glu	ggg Gly	tat Tyr	ccc Pro	tgg Trp	cag Gln	96
agt Ser	ctc Leu	ccg Pro	gag Glu	cag Gln	agt Ser	tcc Ser	gat Asp	gcc Ala	ctg Leu	gaa Glu	gcc Ala	tgg Trp	gag Glu	aat Asn	ggg Gly	144
gag Glu	aga Arg	tcc Ser	cgg Arg	aaa Lys	agg Arg	aga Arg	gca Ala	gtg Val	ctc Leu	acc Thr	caa Gln	aaa Lys	cag Gln	aag Lys	aag Lys	192
cag Gln 65	cac His	tct Ser	gtc Val	ctg Leu	cac His	ctg Leu	gtt Val	ccc Pro	att Ile	aac Asn	gcc Ala	acc Thr	tcc Ser	aag Lys	gat Asp 80	240
gac Asp	tcc Ser	gat Asp	gtg Val	aca Thr 85	gag Glu	gtg Val	atg Met	tgg Trp	caa Gln	cca Pro	gct Ala	ctt Leu	agg Arg	cgt Arg	ggg Gly	288
aga Arg	ggc Gly	cta Leu	cag Gln	gcc Ala	caa Gln	gga Gly	tat Tyr	ggt Gly	gtc Val	cga Arg	atc Ile	cag Gln	gat Asp	gct Ala	gga Gly	336
gtt Val	tat Tyr	ctg Leu	ctg Leu	tat Tyr	agc Ser	cag Gln	gtc Val	ctg Leu	ttt Phe	caa Gln	gac Asp	gtg Val	act Thr	ttc Phe	acc Thr	384
atg Met	ggt Gly	cag Gln	gtg Val	gtg Val	tct Ser	cga Arg	gaa Glu	ggc Gly	caa Gln	gga Gly	agg Arg	cag Gln	gag Glu	act Thr	cta Leu	432
ttc Phe 145	cga Arg	tgt Cys	ata Ile	aga Arg	agt Ser	atg Met	ccc Pro	tcc Ser	cac His	ccg Pro	gac Asp	cgg Arg	gcc Ala	tac Tyr	aac Asn 160	480
agc Ser	tgc Cys	tat Tyr	agc Ser	gca Ala	ggg Gly	gtc Val	ttc Phe	cat His	tta Leu	cac His	caa Gln	ggg Gly	gat Asp	att Ile	ctg Leu	528
agt Ser	gtc Val	ata Ile	att Ile	ccc Pro	cgg Arg	gca Ala	agg Arg	gcg Ala	aaa Lys	ctt Leu	aac Asn	ctc Leu	tct Ser	cca Pro	cat His	576
gga Gly	acc Thr	ttc Phe	ctg Leu	ggg Gly	ttt Phe	gtg Val	aaa Lys	ctg Leu								603

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<210> 37
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 37
 Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu
 1 5 10 15
 Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln
 20 25 30
 Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly
 35 40 45
 Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys
 50 55 60
 Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp
 65 70 75 80
 Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly
 85 90 95
 Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly
 100 105 110
 Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr
 115 120 125
 Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu
 130 135 140
 Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn
 145 150 155 160
 Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
 165 170 175
 Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His
 180 185 190
 Gly Thr Phe Leu Gly Phe Val Lys Leu
 195 200

<210> 38
 <211> 699
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(699)

<400> 38
 atg ggg ggc cca gtc aga gag ccg gca ctc tca gtt gcc ctc tgg ttg 48
 Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu
 1 5 10 15

- 45 -

agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg ctg	96
Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu	
20 25 30	
acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cgg ctg	144
Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu	
35 40 45	
cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg cag	192
Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Tyr Pro Trp Gln	
50 55 60	
agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat ggg	240
Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly	
65 70 75 80	
gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag aag	288
Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys	
85 90 95	
cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag gat	336
Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp	
100 105 110	
gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt ggg	384
Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly	
115 120 125	
aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct gga	432
Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly	
130 135 140	
gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc acc	480
Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr	
145 150 155 160	
atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act cta	528
Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu	
165 170 175	
ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac aac	576
Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn	
180 185 190	
agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att ctg	624
Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu	
195 200 205	
agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca cat	672
Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His	
210 215 220	
gga acc ttc ctg ggg ttt gtg aaa ctg	699
Gly Thr Phe Leu Gly Phe Val Lys Leu	
225 230	

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<210> 39
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 39

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Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu
 1              5              10              15

Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu
              20              25              30

Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu
      35              40              45

Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln
      50              55              60

Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly
      65              70              75              80

Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys
              85              90              95

Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp
      100              105              110

Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly
      115              120              125

Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly
      130              135              140

Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr
      145              150              155              160

Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu
              165              170              175

Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn
      180              185              190

Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
      195              200              205

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His
      210              215              220

Gly Thr Phe Leu Gly Phe Val Lys Leu
      225              230
    
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<210> 40
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(615)

- 47 -

<400> 40
 atg gct ctg ctg acc caa caa aca gag ctg cag agc ctc agg aga gag 48
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu
 1 5 10 15

 gtg agc cgg ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg 96
 Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly
 20 25 30

 tat ccc tgg cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc 144
 Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala
 35 40 45

 tgg gag aat ggg gag aga tcc cgg aaa agg aga gca gtg ctc acc caa 192
 Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln
 50 55 60

 aaa cag aag aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc 240
 Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala
 65 70 75 80

 acc tcc aag gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct 288
 Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala
 85 90 95

 ctt agg cgt ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc 336
 Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile
 100 105 110

 cag gat gct gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac 384
 Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp
 115 120 125

 gtg act ttc acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg 432
 Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg
 130 135 140

 cag gag act cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac 480
 Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp
 145 150 155 160

 cgg gcc tac aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa 528
 Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln
 165 170 175

 ggg gat att ctg agt gtc ata att ccc cgg gca agg gcg aaa ctt aac 576
 Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn
 180 185 190

 ctc tct cca cat gga acc ttc ctg ggg ttt gtg aaa ctg 615
 Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu
 195 200 205

 <210> 41
 <211> 205
 <212> PRT
 <213> Homo sapiens

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<400> 41

Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu
 1 5 10 15
 Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly
 20 25 30
 Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala
 35 40 45
 Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln
 50 55 60
 Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala
 65 70 75 80
 Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala
 85 90 95
 Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile
 100 105 110
 Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp
 115 120 125
 Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg
 130 135 140
 Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp
 145 150 155 160
 Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln
 165 170 175
 Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn
 180 185 190
 Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu
 195 200 205

<210> 42

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence

<220>

<223> Xaas at position 2, 4-6, 12, 13 and 16 may be any
 amino acid

<220>

<223> Any 2 of the Xaas at positions 4-6 may be absent,
 intended to equal a range of 1-3;

<220>

<223> Any 1 of the Xaas at positions 12-13 may be absent,
intended to equal a range of 1-2;

<400> 42

Val Xaa Ile Xaa Xaa Xaa Gly Val Tyr Leu Leu Xaa Xaa Glu Val Xaa
1 5 10 15

Phe

<210> 43

<211> 233

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195 200 205

- 50 -

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 44
<211> 249
<212> PRT
<213> Homo sapiens

<400> 44
Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro
1 5 10 15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu
20 25 30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala
35 40 45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu
50 55 60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp
65 70 75 80

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro
85 90 95

Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala His Tyr Glu
100 105 110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly
115 120 125

Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu
130 135 140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu
145 150 155 160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr
165 170 175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu
180 185 190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg
195 200 205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu
210 215 220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His
245

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<210> 45
 <211> 1119
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (140)..(871)

<400> 45

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gtcgacccac gcgtccggca ggatgtttgc agtgtcgcgc ccagggctct gagactgagc 60
ctgccatcca ctgcacgcc tttctttcag ggcttttcgg ctgttggtta cactgatgtg 120
acccccctcc ctttttggga atg atg ggg atc ttt ttg gtg tat gtt gga ttt 172
      Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe
      1               5               10

gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt tct tct caa gca 220
Val Phe Phe Ser Val Leu Tyr Val Gln Gly Leu Ser Ser Gln Ala
      15               20               25

aaa ttt acc gag ttt ccg cgg aac gtg acg gcg acc gag ggg cag aat 268
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn
      30               35               40

gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg 316
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu
      45               50               55

gag atc caa tgg tgg ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg 364
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly
      60               65               70               75

gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga gac ccg 412
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro
      80               85               90

gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc aat gac 460
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp
      95               100              105

atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat gaa ggc 508
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly
      110              115              120

tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt cag gaa 556
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu
      125              130              135

cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gcc cgc 604
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg
      140              145              150              155

aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat atg aag 652
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys
      160              165              170

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ccc cgc aag aac gtc tcc gca gcc atc ccc agc agc atc cat ggc tct 700
 Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser
 175 180 185

gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta gcc aaa 748
 Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys
 190 195 200

atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc gag cct 796
 Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro
 205 210 215

ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg tat aga 844
 Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg
 220 225 230 235

gta gac aga ttt atg aat ggt gat ttt taaaatcgga gacctagttc 891
 Val Asp Arg Phe Met Asn Gly Asp Phe
 240

agtgcagtgt attatgagag gtgagcactg agcctgcacc aattcactca gagctcaaag 951

catgtgggtg caccctgtca gtcccctagt ggtgcttcat ttccagggca tctgagagct 1011

ggactctggt ttttatcctt tctgtattta cacattataa gaacaataaa tcatgtaatg 1071

ttggttacat tacaaaaaaaa aaaaaaaaaa aaaaaaaagg gcggccgc 1119

<210> 46

<211> 244

<212> PRT

<213> Homo sapiens

<400> 46

Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val
 1 5 10 15

Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Phe
 20 25 30

Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys
 35 40 45

Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp
 50 55 60

Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly
 65 70 75 80

Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr
 85 90 95

Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu
 100 105 110

Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg
 115 120 125

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Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala
 130 135 140

Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe
 145 150 155 160

Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys Pro Arg Lys Asn Val
 165 170 175

Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser Ala Asn Gln Arg Thr
 180 185 190

His Ser Thr Ser Ser Pro Gln Val Val Ala Lys Ile Pro Lys Gln Ser
 195 200 205

Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro Phe Ile Leu Pro Leu
 210 215 220

Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg Val Asp Arg Phe Met
 225 230 235 240

Asn Gly Asp Phe

<210> 47
 <211> 735
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(732)

<400> 47
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 Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val
 1 5 10 15

tta tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttt 96
 Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Phe
 20 25 30

ccg cgg aac gtg acg gcg acc gag ggg cag aat gtg gag atg tcc tgc 144
 Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys
 35 40 45

gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg gag atc caa tgg tgg 192
 Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp
 50 55 60

ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg gcc gag ggg gcc ggc 240
 Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly
 65 70 75 80

gcg cag gtg gag ctc ttg ccc gac aga gac ccg gac agc gac ggg acc 288
 Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr
 85 90 95

- 54 -

aag atc agc aca gtg aaa gtc caa ggc aat gac atc tcc cac aag ctt 336
Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu
100 105 110
cag att tcc aaa gtg agg aaa aag gat gaa ggc tta tat gag tgc agg 384
Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg
115 120 125
gtg act gat gcc aac tac ggg gag ctt cag gaa cac aag gcc cag gcc 432
Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala
130 135 140
tat ctg aaa gtc aat gcc aac agc cat gcc cgc aga atg cag gcc ttc 480
Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe
145 150 155 160
gaa gcc tcg ccc atg tgg ctg cag gat atg aag ccc cgc aag aac gtc 528
Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys Pro Arg Lys Asn Val
165 170 175
tcc gca gcc atc ccc agc agc atc cat ggc tct gcc aac caa cga acg 576
Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser Ala Asn Gln Arg Thr
180 185 190
cac tcc acc tcc agc cct caa gtg gta gcc aaa atc ccc aaa caa agt 624
His Ser Thr Ser Ser Pro Gln Val Val Ala Lys Ile Pro Lys Gln Ser
195 200 205
cca caa tca ggt atg gaa acc cat ttc gag cct ttt att tta cca ctc 672
Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro Phe Ile Leu Pro Leu
210 215 220
aca aac gct cca cag aaa ggt cag tcg tat aga gta gac aga ttt atg 720
Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg Val Asp Arg Phe Met
225 230 235 240
aat ggt gat ttt taa 735
Asn Gly Asp Phe

<210> 48
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(657)

<400> 48
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Gln Ala Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly
1 5 10 15
cag aat gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg 96
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
20 25 30

tat	ctg	gag	atc	caa	tgg	tgg	ttc	ctg	cgg	ggg	ccg	gag	gac	ctg	gat	144
Tyr	Leu	Glu	Ile	Gln	Trp	Trp	Phe	Leu	Arg	Gly	Pro	Glu	Asp	Leu	Asp	
		35					40					45				

ccc ggg gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga 192
 Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg
 50 - 55 60

gac ccg gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc 240
Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
65 70 75 80

aat gac atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat 288
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
85 90 95

gaa ggc tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt 336
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
100 105 110

cag gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat 384
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
115 120 125

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gcc cgc aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat 432
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
      130                135                140
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atg	aag	ccc	cgc	aag	aac	gtc	tcc	gca	gcc	atc	ccc	agc	agc	atc	cat	480
Met	Lys	Pro	Arg	Lys	Asn	Val	Ser	Ala	Ala	Ile	Pro	Ser	Ser	Ile	His	
145					150					155					160	

ggc tct gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta 528
Gly Ser Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val
165 170 175

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gcc aaa atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc    576
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe
      180                      185                      190
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gag cct ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg 624
Glu Pro Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser
195 200 205

tat	aga	gta	gac	aga	ttt	atg	aat	ggg	gat	ttt	taa	
Tyr	Arg	Val	Asp	Arg	Phe	Met	Asn	Gly	Asp	Phe		660
	210				215							

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<210> 49
<211> 219
<212> PRT
<213> Homo sapiens
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<400> 49
Gln Ala Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly
1 5 10 15

Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
20 25 30



10

10

10

- 57 -

ttt atg ttc ttt tcc gtg tta tat gta caa caa ggg ctt tct tct caa	342
Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln	
10 15 20 25	
gca aaa ttt acc gag ttg ccg aga aat gtg act gct acc gaa ggg caa	390
Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly Gln	
30 35 40	
aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg tac	438
Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr	
45 50 55	
ctg gag atc cag tgg tgg ttc ctt cgg ggg cca gag gac ctg gag caa	486
Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu Gln	
60 65 70	
ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga gac	534
Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg Asp	
75 80 85	
ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc aat	582
Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn	
90 95 100 105	
gat atc tcc cac aag ctt cag ata tcc aaa gtg aga aaa aag gat gaa	630
Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu	
110 115 120	
ggt tta tac gag tgc agg gtg act gac gct aac tac ggg gag ctt cag	678
Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln	
125 130 135	
gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gct	726
Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala	
140 145 150	
cgg agg atg cag gcc ttt gaa gcc tca cct atg tgg ctg caa gac acg	774
Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Thr	
155 160 165	
aag cct cga aag aac gca tca tcg gtg gtt ccc agc agc gtc cac aac	822
Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His Asn	
170 175 180 185	
tct gcc aac caa cga atg cac tcc acc tcc agc cct caa gcg gta gcc	870
Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val Ala	
190 195 200	
aaa atc ccc aag caa agt cca caa tca gca aag agc aaa tcg cct gta	918
Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro Val	
205 210 215	
aaa tct acg gag cgg aca gca aag ttg acc cta tac tcc aag cac cat	966
Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His His	
220 225 230	
tct gca ccc ctg tac tct agt tat cta cac aag gag cat cag ctt ccg	1014
Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu Pro	
235 240 245	

- 58 -

gaa gca taagtgaaga cactgtcaca cgctttattg ataatatattt ctttggaag 1070
Glu Ala
250

ttgctgatct tttatttcaa gagaattaat gggaagagat aggacatttt ccaattacaa 1130
gaccaatttt tttcctttta tttcaacaaa taaaacctgc atttactga ctgctcagga 1190
gttggcctga atgacatcag tataactaaat atttccatgg attccaccaa tttcctaacg 1250
agggacacct aatcttcaag aagcaacaaa agatggaaaa cctaagaacc acaaactgtc 1310
tcatacagca cccagctga ggaacaaaac aaatagctaa atgctgacca tggcaaatca 1370
acatcagaca actttatttt acatatggaa taatcaaaga aagttttttt tttacttcct 1430
ttttgcccc tggaatttat cttggagttt cctttttttc cttgattgcc gttttcgttc 1490
aatggtagca agtgccaatt atggccaatc cttgtcaatc ctggaagggt tatattcata 1550
tacattgagt gtggtatata tcaatgtatt ttaattcatt tggcaatttc tgtataggca 1610
aacctggcaa attctgtaaa ttgcttatag tatgtgtgat atgacttcaa ggtagatagg 1670
ctatgatgct catgcaagct gactttcttc attctatata caaatatatt catgagcata 1730
tattaggcca ccaacttctt ttctaaaga attatttttc atttgtacct catgtatttt 1790
gtgaattttg tagtatattt ctctgttcca ctagtttgac cgctacagtt tgtctctgtt 1850
gtcctctact tcttctgga aaaatttaaa attgtgtatg tctctgataa atgaattaat 1910
tttgttgtgt gtatgctatg ttggaatttg ctgtgttctt ttaaacatgt atttattaag 1970
gtttggggat cttgagttga gtctgaagaa tgcacacctg gtttttgaca gagttcctca 2030
tgttaccaat attctatctc agagaaagaa agacaccaag tgggaaaact aagaagacat 2090
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aatgtctact aattaaaaat taaaatgtga ttgttgctg aatacaatat gcaaatgact 2270
gcaaagccca tactgaagaa aatagatgtt taatcttcac tcaataatta taattttaaa 2330
tagttcatca ttattttttg accttatgat attttgttta gacctgttct aattacatct 2390
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aaaccagaaa ccatatatgt aggaatgggt cattcctaata gtaaggccat aaattgtagc 2570
ttgaaggcaa ggaatacatt tgttttttta tggtaaagga ctggcctctg acatgcactt 2630
ataagcaatg tgaatatattt cataatatgc ttgacattct cttttaacaa atattgtttt 2690
atggtaaatac tttccttgcc atttttcttc tttcatttga ttcattattt cattctaatag 2750

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aagaaaataa aggtttaatt atgatacttt attaacatac aaatgtattt tctttctaag 2810
 ttaaataatct gaaagttgta taaaatgatg gtagagaaat attactcatt cggtttcttt 2870
 gagctttaag aatcccatatc attgcagtat atattagaat actgatttaa catcaaactg 2930
 ggggggaaaa tcatgtatta tactttttact caatgtctag gtaatggatt cagctaattt 2990
 tacagcaagc caaatgtgta cccgtatcag taatgttcac catgcttgta ataaaagggc 3050
 atatgctagt tttggaagaa tgctcattag attcattgta tcagtgtcca aaataataaa 3110
 gacctgttta tcaactgtgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3170
 aaaaaaaaaa aaaaaagggc ggccgc 3196

<210> 51
 <211> 251
 <212> PRT
 <213> Mus musculus

<400> 51
 Met Gly Ile Phe Leu Ala Ser Val Gly Phe Met Phe Phe Ser Val Leu
 1 5 10 15
 Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Leu Pro
 20 25 30
 Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala
 35 40 45
 Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe
 50 55 60
 Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser
 65 70 75 80
 Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys
 85 90 95
 Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln
 100 105 110
 Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg Val
 115 120 125
 Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala Tyr
 130 135 140
 Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe Glu
 145 150 155 160
 Ala Ser Pro Met Trp Leu Gln Asp Thr Lys Pro Arg Lys Asn Ala Ser
 165 170 175
 Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gln Arg Met His
 180 185 190

- 60 -

Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro
195 200 205

Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala
210 215 220

Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser
225 230 235 240

Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala
245 250

<210> 52
<211> 756
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(753)

<400> 52
atg ggg atc ttt ttg gcg tct gtt gga ttt atg ttc ttt tcc gtg tta 48
Met Gly Ile Phe Leu Ala Ser Val Gly Phe Met Phe Phe Ser Val Leu
1 5 10 15
tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttg ccg 96
Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Leu Pro
20 25 30
aga aat gtg act gct acc gaa ggg caa aat gtg gag atg tcc tgt gct 144
Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala
35 40 45
ttc caa agc ggc tct gct tca gtg tac ctg gag atc cag tgg tgg ttc 192
Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe
50 55 60
ctt cgg ggg cca gag gac ctg gag caa ggc acg gag gct gca ggc tcg 240
Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser
65 70 75 80
cag gtg gag ctc tta ccc gac aga gac ccg gac aac gat ggg acc aag 288
Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys
85 90 95
att agt aca gtg aaa gtc caa ggc aat gat atc tcc cac aag ctt cag 336
Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln
100 105 110
ata tcc aaa gtg aga aaa aag gat gaa ggt tta tac gag tgc agg gtg 384
Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg Val
115 120 125
act gac gct aac tac ggg gag ctt cag gaa cac aag gcc cag gcc tat 432
Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala Tyr
130 135 140

- 61 -

ctg aaa gtc aat gcc aac agc cat gct cgg agg atg cag gcc ttt gaa 480
 Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe Glu
 145 150 155 160

gcc tca cct atg tgg ctg caa gac acg aag cct cga aag aac gca tca 528
 Ala Ser Pro Met Trp Leu Gln Asp Thr Lys Pro Arg Lys Asn Ala Ser
 165 170 175

tcg gtg gtt ccc agc agc gtc cac aac tct gcc aac caa cga atg cac 576
 Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gln Arg Met His
 180 185 190

tcc acc tcc agc cct caa gcg gta gcc aaa atc ccc aag caa agt cca 624
 Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro
 195 200 205

caa tca gca aag agc aaa tcg cct gta aaa tct acg gag cgg aca gca 672
 Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala
 210 215 220

aag ttg acc cta tac tcc aag cac cat tct gca ccc ctg tac tct agt 720
 Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser
 225 230 235 240

tat cta cac aag gag cat cag ctt ccg gaa gca taa 756
 Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala
 245 250

<210> 53
 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(681)

<400> 53
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 Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly
 1 5 10 15

caa aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg 96
 Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
 20 25 30

tac ctg gag atc cag tgg tgg ttc ctt cgg ggg cca gag gac ctg gag 144
 Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu
 35 40 45

caa ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga 192
 Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
 50 55 60

gac ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc 240
 Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
 65 70 75 80

Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
50 55 60

- 63 -

Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
 65 70 75 80
 Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
 85 90 95
 Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
 100 105 110
 Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
 115 120 125
 Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
 130 135 140
 Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His
 145 150 155 160
 Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val
 165 170 175
 Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro
 180 185 190
 Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His
 195 200 205
 His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu
 210 215 220
 Pro Glu Ala
 225

<210> 55
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 55
 Gly Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser
 1 5 10 15
 Val Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu
 20 25 30
 Asp Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp
 35 40 45
 Arg Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln
 50 55 60
 Gly Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys
 65 70 75 80
 Asp Glu Gly Leu Tyr Glu Cys Arg Val
 85

- 64 -

<210> 56
<211> 89
<212> PRT
<213> Mus musculus

<400> 56
Gly Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser
1 5 10 15
Val Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu
20 25 30
Glu Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp
35 40 45
Arg Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln
50 55 60
Gly Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys
65 70 75 80
Asp Glu Gly Leu Tyr Glu Cys Arg Val
85

<210> 57
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 57
Gly Gln Ser Val Thr Leu Thr Cys Met Val Ser Phe His Pro Pro Asp
1 5 10 15
Tyr Thr Ile Trp Trp Tyr Arg Asn Gly Gln Pro Ile Thr Leu Thr Ile
20 25 30
Asn Ser Trp Gln Tyr Glu Asp Ser Glu Thr Tyr Trp Cys Met Val
35 40 45

<210> 58
<211> 2852
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (160)..(2178)

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gtcgacccac gcgtccggag cccggggcgg gtggacgcgg actcgaacgc agttgcttcg 60
ggacccagga cccctcggg cccgacccgc caggaaagac tgaggccgcg gcctgccccg 120

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cccggctccc tgcgccgcgcg ccgcctcccg ggacagaag atg tgc tcc agg gtc	174
Met Cys Ser Arg Val	
1 5	
cct ctg ctg ctg ccg ctg ctc ctg cta ctg gcc ctg ggg cct ggg gtg	222
Pro Leu Leu Leu Pro Leu Leu Leu Leu Ala Leu Gly Pro Gly Val	
10 15 20	
cag ggc tgc cca tcc ggc tgc cag tgc agc cag cca cag aca gtc ttc	270
Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln Pro Gln Thr Val Phe	
25 30 35	
tgc act gcc cgc cag ggg acc acg gtg ccc cga gac gtg cca ccc gac	318
Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg Asp Val Pro Pro Asp	
40 45 50	
acg gtg ggg ctg tac gtc ttt gag aac ggc atc acc atg ctc gac gca	366
Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile Thr Met Leu Asp Ala	
55 60 65	
ggc agc ttt gcc ggc ctg ccg ggc ctg cag ctc ctg gac ctg tca cag	414
Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln	
70 75 80 85	
aac cag atc gcc agc ctg ccc agc ggg gtc ttc cag cca ctc gcc aac	462
Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe Gln Pro Leu Ala Asn	
90 95 100	
ctc agc aac ctg gac ctg acg gcc aac agg ctg cat gaa atc acc aat	510
Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu His Glu Ile Thr Asn	
105 110 115	
gag acc ttc cgt ggc ctg cgg cgc ctc gag cgc ctc tac ctg ggc aag	558
Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys	
120 125 130	
aac cgc atc cgc cac atc cag cct ggt gcc ttc gac acg ctc gac cgc	606
Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg	
135 140 145	
ctc ctg gag ctc aag ctg cag gac aac gag ctg cgg gca ctg ccc ccg	654
Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu Arg Ala Leu Pro Pro	
150 155 160 165	
ctg cgc ctg ccc cgc ctg ctg ctg ctg gac ctc agc cac aac agc ctc	702
Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser Leu	
170 175 180	
ctg gcc ctg gag ccc ggc atc ctg gac act gcc aac gtg gag gcg ctg	750
Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu Ala Leu	
185 190 195	
cgg ctg gct ggt ctg ggg ctg cag cag ctg gac gag ggg ctc ttc agc	798
Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly Leu Phe Ser	
200 205 210	
cgc ttg cgc aac ctc cac gac ctg gat gtg tcc gac aac cag ctg gag	846
Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp Asn Gln Leu Glu	
215 220 225	

- 66 -

cga	gtg	cca	cct	gtg	atc	cga	ggc	ctc	cgg	ggc	ctg	acg	cgc	ctg	cgg	894
Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly	Leu	Thr	Arg	Leu	Arg	
230					235					240					245	
ctg	gcc	ggc	aac	acc	cgc	att	gcc	cag	ctg	cgg	ccc	gag	gac	ctg	gcc	942
Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu	Arg	Pro	Glu	Asp	Leu	Ala	
				250					255						260	
ggc	ctg	gct	gcc	ctg	cag	gag	ctg	gat	gtg	agc	aac	cta	agc	ctg	cag	990
Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp	Val	Ser	Asn	Leu	Ser	Leu	Gln	
			265					270						275		
gcc	ctg	cct	ggc	gac	ctc	tgc	ggc	ctc	ttc	ccc	cgc	ctg	cgg	ctg	ctg	1038
Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly	Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	
		280					285						290			
gca	gct	ggc	cgc	aac	ccc	ttc	aac	tgc	gtg	tgc	ccc	ctg	agc	tgg	ttt	1086
Ala	Ala	Ala	Arg	Asn	Pro	Phe	Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	
	295					300					305					
ggc	ccc	tgg	gtg	cgc	gag	agc	cac	gtc	aca	ctg	gcc	agc	cct	gag	gag	1134
Gly	Pro	Trp	Val	Arg	Glu	Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	
310					315					320					325	
acg	cgc	tgc	cac	ttc	ccg	ccc	aag	aac	gct	ggc	cgg	ctg	ctc	ctg	gag	1182
Thr	Arg	Cys	His	Phe	Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	
				330					335						340	
ctt	gac	tac	gcc	gac	ttt	ggc	tgc	cca	gcc	acc	acc	acc	aca	gcc	aca	1230
Leu	Asp	Tyr	Ala	Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	
			345					350						355		
gtg	ccc	acc	acg	agg	ccc	gtg	gtg	cgg	gag	ccc	aca	gcc	ttg	tct	tct	1278
Val	Pro	Thr	Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	
		360					365						370			
agc	ttg	gct	cct	acc	tgg	ctt	agc	ccc	aca	gcg	ccg	gcc	act	gag	gcc	1326
Ser	Leu	Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	
	375					380					385					
ccc	agc	ccg	ccc	tcc	act	gcc	cca	ccg	act	gta	ggg	cct	gtc	ccc	cag	1374
Pro	Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln	
390					395					400					405	
ccc	cag	gac	tgc	cca	ccg	tcc	acc	tgc	ctc	aat	ggg	ggc	aca	tgc	cac	1422
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys	His	
				410					415						420	
ctg	ggg	aca	cgg	cac	cac	ctg	gcg	tgc	ttg	tgc	ccc	gaa	ggc	ttc	acg	1470
Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly	Phe	Thr	
			425					430						435		
ggc	ctg	tac	tgt	gag	agc	cag	atg	ggg	cag	ggg	aca	cgg	ccc	agc	cct	1518
Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg	Pro	Ser	Pro	
		440					445						450			
aca	cca	gtc	acg	ccg	agg	cca	cca	cgg	tcc	ctg	acc	ctg	ggc	atc	gag	1566
Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr	Leu	Gly	Ile	Glu	
	455					460					465					

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ccg gtg agc ccc acc tcc ctg cgc gtg ggg ctg cag cgc tac ctc cag	1614
Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu Gln Arg Tyr Leu Gln	
470 475 480 485	
ggg agc tcc gtg cag ctc agg agc ctc cgt ctc acc tat cgc aac cta	1662
Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu	
490 495 500	
tcg ggc cct gat aag cgg ctg gtg acg ctg cga ctg cct gcc tcg ctc	1710
Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg Leu Pro Ala Ser Leu	
505 510 515	
gct gag tac acg gtc acc cag ctg cgg ccc aac gcc act tac tcc gtc	1758
Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn Ala Thr Tyr Ser Val	
520 525 530	
tgt gtc atg cct ttg ggg ccc ggg cgg gtg ccg gag ggc gag gag gcc	1806
Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro Glu Gly Glu Glu Ala	
535 540 545	
tgc ggg gag gcc cat aca ccc cca gcc gtc cac tcc aac cac gcc cca	1854
Cys Gly Glu Ala His Thr Pro Pro Ala Val His Ser Asn His Ala Pro	
550 555 560 565	
gtc acc cag gcc cgc gag ggc aac ctg ccg ctc ctc att gcg ccc gcc	1902
Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala	
570 575 580	
ctg gcc gcg gtg ctc ctg gcc gcg ctg gct gcg gtg ggg gca gcc tac	1950
Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr	
585 590 595	
tgt gtg cgg cgg ggg cgg gcc atg gca gca gcg gct cag gac aaa ggg	1998
Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly	
600 605 610	
cag gtg ggg cca ggg gct ggg ccc ctg gaa ctg gag gga gtg aag gtc	2046
Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val	
615 620 625	
ccc ttg gag cca ggc ccg aag gca aca gag ggc ggt gga gag gcc ctg	2094
Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu	
630 635 640 645	
ccc agc ggg tct gag tgt gag gtg cca ctc atg ggc ttc cca ggg cct	2142
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly Pro	
650 655 660	
ggc ctc cag tca ccc ctc cac gca aag ccc tac atc taagccagag	2188
Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile	
665 670	
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ccacaccacg taagttctca gtcccaacct cggggatgtg tgcagacagg gctgtgtgac	2308
cacagctggg ccctgttccc tctggacctc ggtctcctca tctgtgagat gctgtggccc	2368
agctgacgag ccctaacgtc ccagaaaccg agtgcctatg aggacagtgt ccgccctgcc	2428

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ctccgcaacg tgcagtcctt gggcacggcg ggccttgcca tgtgctggta acgcatgcct 2488
 gggccctgct gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2548
 gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttggc cccaggaagc 2608
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 ccgc 2852

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<211> 673

<212> PRT

<213> Homo sapiens

<400> 59

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Leu	Gly	Pro	Gly	Val	Gln	Gly	Cys	Pro	Ser	Gly	Cys	Gln	Cys	Ser	Gln	20	25	30
Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr	Val	Pro	Arg	35	40	45
Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe	Glu	Asn	Gly	Ile	50	55	60
Thr	Met	Leu	Asp	Ala	Gly	Ser	Phe	Ala	Gly	Leu	Pro	Gly	Leu	Gln	Leu	65	70	75
Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser	Leu	Pro	Ser	Gly	Val	Phe	85	90	95
Gln	Pro	Leu	Ala	Asn	Leu	Ser	Asn	Leu	Asp	Leu	Thr	Ala	Asn	Arg	Leu	100	105	110
His	Glu	Ile	Thr	Asn	Glu	Thr	Phe	Arg	Gly	Leu	Arg	Arg	Leu	Glu	Arg	115	120	125
Leu	Tyr	Leu	Gly	Lys	Asn	Arg	Ile	Arg	His	Ile	Gln	Pro	Gly	Ala	Phe	130	135	140
Asp	Thr	Leu	Asp	Arg	Leu	Leu	Glu	Leu	Lys	Leu	Gln	Asp	Asn	Glu	Leu	145	150	155
Arg	Ala	Leu	Pro	Pro	Leu	Arg	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Asp	Leu	165	170	175
Ser	His	Asn	Ser	Leu	Leu	Ala	Leu	Glu	Pro	Gly	Ile	Leu	Asp	Thr	Ala	180	185	190

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Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp
 195 200 205
 Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser
 210 215 220
 Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly
 225 230 235 240
 Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg
 245 250 255
 Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser
 260 265 270
 Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro
 275 280 285
 Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys
 290 295 300
 Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu
 305 310 315 320
 Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly
 325 330 335
 Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr
 340 345 350
 Thr Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro
 355 360 365
 Thr Ala Leu Ser Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala
 370 375 380
 Pro Ala Thr Glu Ala Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val
 385 390 395 400
 Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn
 405 410 415
 Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys
 420 425 430
 Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly
 435 440 445
 Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu
 450 455 460
 Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu
 465 470 475 480
 Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu
 485 490 495
 Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg
 500 505 510

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Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn
515 520 525

Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro
530 535 540

Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His
545 550 555 560

Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu
565 570 575

Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala
580 585 590

Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala
595 600 605

Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu
610 615 620

Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly
625 630 635 640

Gly Gly Glu Ala Leu Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met
645 650 655

Gly Phe Pro Gly Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr
660 665 670

Ile

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<213> Homo sapiens

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Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu Ala
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ctg ggg cct ggg gtg cag ggc tgc cca tcc ggc tgc cag tgc agc cag 96
Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln
20 25 30

cca cag aca gtc ttc tgc act gcc cgc cag ggg acc acg gtg ccc cga 144
Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg
35 40 45

gac gtg cca ccc gac acg gtg ggg ctg tac gtc ttt gag aac ggc atc 192
Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile
50 55 60

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acc atg ctc gac gca ggc agc ttt gcc ggc ctg ccg ggc ctg cag ctc	240
Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu	
65 70 75 80	
ctg gac ctg tca cag aac cag atc gcc agc ctg ccc agc ggg gtc ttc	288
Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe	
85 90 95	
cag cca ctc gcc aac ctc agc aac ctg gac ctg acg gcc aac agg ctg	336
Gln Pro Leu Ala Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu	
100 105 110	
cat gaa atc acc aat gag acc ttc cgt ggc ctg cgg cgc ctc gag cgc	384
His Glu Ile Thr Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg	
115 120 125	
ctc tac ctg ggc aag aac cgc atc cgc cac atc cag cct ggt gcc ttc	432
Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe	
130 135 140	
gac acg ctc gac cgc ctc ctg gag ctc aag ctg cag gac aac gag ctg	480
Asp Thr Leu Asp Arg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu	
145 150 155 160	
cgg gca ctg ccc ccg ctg cgc ctg ccc cgc ctg ctg ctg ctg gac ctc	528
Arg Ala Leu Pro Pro Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu	
165 170 175	
agc cac aac agc ctc ctg gcc ctg gag ccc ggc atc ctg gac act gcc	576
Ser His Asn Ser Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala	
180 185 190	
aac gtg gag gcg ctg cgg ctg gct ggt ctg ggg ctg cag cag ctg gac	624
Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp	
195 200 205	
gag ggg ctc ttc agc cgc ttg cgc aac ctc cac gac ctg gat gtg tcc	672
Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser	
210 215 220	
gac aac cag ctg gag cga gtg cca cct gtg atc cga ggc ctc cgg ggc	720
Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly	
225 230 235 240	
ctg acg cgc ctg cgg ctg gcc ggc aac acc cgc att gcc cag ctg cgg	768
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg	
245 250 255	
ccc gag gac ctg gcc ggc ctg gct gcc ctg cag gag ctg gat gtg agc	816
Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser	
260 265 270	
aac cta agc ctg cag gcc ctg cct ggc gac ctc tcg ggc ctc ttc ccc	864
Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro	
275 280 285	
cgc ctg cgg ctg ctg gca gct gcc cgc aac ccc ttc aac tgc gty tgc	912
Arg Leu Arg Leu Leu Ala Ala Arg Asn Pro Phe Asn Cys Val Cys	
290 295 300	

ccc ctg agc tgg ttt ggc ccc tgg gtg cgc gag agc cac gtc aca ctg	960
Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu	
305 310 315 320	
gcc agc cct gag gag acg cgc tgc cac ttc ccg ccc aag aac gct ggc	1008
Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly	
325 330 335	
cgg ctg ctc ctg gag ctt gac tac gcc gac ttt ggc tgc cca gcc acc	1056
Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr	
340 345 350	
acc acc aca gcc aca gtg ccc acc acg agg ccc gtg gtg cgg gag ccc	1104
Thr Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro	
355 360 365	
aca gcc ttg tct tct agc ttg gct cct acc tgg ctt agc ccc aca gcg	1152
Thr Ala Leu Ser Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala	
370 375 380	
ccg gcc act gag gcc ccc agc ccg ccc tcc act gcc cca ccg act gta	1200
Pro Ala Thr Glu Ala Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val	
385 390 395 400	
ggg cct gtc ccc cag ccc cag gac tgc cca ccg tcc acc tgc ctc aat	1248
Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn	
405 410 415	
ggg ggc aca tgc cac ctg ggg aca cgg cac cac ctg gcg tgc ttg tgc	1296
Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys	
420 425 430	
ccc gaa ggc ttc acg ggc ctg tac tgt gag agc cag atg ggg cag ggg	1344
Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly	
435 440 445	
aca cgg ccc agc cct aca cca gtc acg ccg agg cca cca cgg tcc ctg	1392
Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu	
450 455 460	
acc ctg ggc atc gag ccg gtg agc ccc acc tcc ctg cgc gtg ggg ctg	1440
Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu	
465 470 475 480	
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Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu	
485 490 495	
acc tat cgc aac cta tcg ggc cct gat aag cgg ctg gtg acg ctg cga	1536
Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg	
500 505 510	
ctg cct gcc tcg ctc gct gag tac acg gtc acc cag ctg cgg ccc aac	1584
Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn	
515 520 525	
gcc act tac tcc gtc tgt gtc atg cct ttg ggg ccc ggg cgg gtg ccg	1632
Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro	
530 535 540	

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gag ggc gag gag ggc tgc ggg gag gcc cat aca ccc cca gcc gtc cac	1680
Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His	
545 550 555 560	
tcc aac cac gcc cca gtc acc cag gcc cgc gag ggc aac ctg ccg ctc	1728
Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu	
565 570 575	
ctc att gcg ccc gcc ctg gcc gcg gtg ctc ctg gcc gcg ctg gct gcg	1776
Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala	
580 585 590	
gtg ggg gca gcc tac tgt gtg cgg cgg ggg cgg gcc atg gca gca gcg	1824
Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala	
595 600 605	
gct cag gac aaa ggg cag gtg ggg cca ggg gct ggg ccc ctg gaa ctg	1872
Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu	
610 615 620	
gag gga gtg aag gtc ccc ttg gag cca ggc ccg aag gca aca gag ggc	1920
Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly	
625 630 635 640	
ggt gga gag gcc ctg ccc agc ggg tct gag tgt gag gtg cca ctc atg	1968
Gly Gly Glu Ala Leu Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met	
645 650 655	
ggc ttc cca ggg cct ggc ctc cag tca ccc ctc cac gca aag ccc tac	2016
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660 665 670	
atc	2019
Ile	

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 <212> PRT
 <213> Homo sapiens

<400> 61
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 35 40 45
 Pro Thr Asn Leu Thr His Ile Leu Leu Phe Gly Met Gly Arg Gly Val
 50 55 60
 Leu Gln Ser Gln Ser Phe Ser Gly Met Thr Val Leu Gln Arg Leu Met
 65 70 75 80
 Ile Ser Asp Ser His Ile Ser Ala Val Ala Pro Gly Thr Phe Ser Asp
 85 90 95

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Leu Ile Lys Leu Lys Thr Leu Arg Leu Ser Arg Asn Lys Ile Thr His
100 105 110

Leu Pro Gly Ala Leu Leu Asp Lys Met Val Leu Leu Glu Gln Leu Phe
115 120 125

Leu Asp His Asn Ala Leu Arg Gly Ile Asp Gln Asn Met Phe Gln Lys
130 135 140

Leu Val Asn Leu Gln Glu Leu Ala Leu Asn Gln Asn Gln Leu Asp Phe
145 150 155 160

Leu Pro Ala Ser Leu Phe Thr Asn Leu Glu Asn Leu Lys Leu Leu Asp
165 170 175

Leu Ser Gly Asn Asn Leu Thr His Leu Pro Lys Gly Leu Leu Gly Ala
180 185 190

Gln Ala Lys Leu Glu Arg Leu Leu Leu His Ser Asn Arg Leu Val Ser
195 200 205

Leu Asp Ser Gly Leu Leu Asn Ser Leu Gly Ala Leu Thr Glu Leu Gln
210 215 220

Phe His Arg Asn His Ile Arg Ser Ile Ala Pro Gly Ala Phe Asp Arg
225 230 235 240

Leu Pro Asn Leu Ser Ser Leu Thr Leu Ser Arg Asn His Leu Ala Phe
245 250 255

Leu Pro Ser Ala Leu Phe Leu His Ser His Asn Leu Thr Leu Leu Thr
260 265 270

Leu Phe Glu Asn Pro Leu Ala Glu Leu Pro Gly Val Leu Phe Gly Glu
275 280 285

Met Gly Gly Leu Gln Glu Leu Trp Leu Asn Arg Thr Gln Leu Arg Thr
290 295 300

Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Arg Leu Arg Tyr Leu Gly
305 310 315 320

Val Thr Leu Ser Pro Arg Leu Ser Ala Leu Pro Gln Gly Ala Phe Gln
325 330 335

Gly Leu Gly Glu Leu Gln Val Leu Ala Leu His Ser Asn Gly Leu Thr
340 345 350

Ala Leu Pro Asp Gly Leu Leu Arg Gly Leu Gly Lys Leu Arg Gln Val
355 360 365

Ser Leu Arg Arg Asn Arg Leu Arg Ala Leu Pro Arg Ala Leu Phe Arg
370 375 380

Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Asp His Asn Gln Leu Glu
385 390 395 400

Thr Leu Pro Gly Asp Val Phe Gly Ala Leu Pro Arg Leu Thr Glu Val
405 410 415

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Leu Leu Gly His Asn Ser Trp Arg Cys Asp Cys Gly Leu Gly Pro Phe
420 425 430

Leu Gly Trp Leu Arg Gln His Leu Gly Leu Val Gly Gly Glu Glu Pro
435 440 445

Pro Arg Cys Ala Gly Pro Gly Ala His Ala Gly Leu Pro Leu Trp Ala
450 455 460

Leu Pro Gly Gly Asp Ala Glu Cys Pro Gly Pro Arg Gly Pro Pro Pro
465 470 475 480

Arg Pro Ala Ala Asp Ser Ser Ser Glu Ala Pro Val His Pro Ala Leu
485 490 495

Ala Pro Asn Ser Ser Glu Pro Trp Val Trp Ala Gln Pro Val Thr Thr
500 505 510

Gly Lys Gly Gln Asp His Ser Pro Phe Trp Gly Phe Tyr Phe Leu Leu
515 520 525

Leu Ala Val Gln Ala Met Ile Thr Val Ile Ile Val Phe Ala Met Ile
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35 40 45

Tyr Asp Asp Glu Val Asn Glu Leu Ser Val Phe Cys Ser Ser Arg Asn
50 55 60

Leu Thr Arg Leu Pro Asp Gly Ile Pro Gly Gly Thr Gln Ala Leu Trp
65 70 75 80

Leu Asp Ser Asn Asn Leu Ser Ser Ile Pro Pro Ala Ala Phe Arg Asn
85 90 95

Leu Ser Ser Leu Ala Phe Leu Asn Leu Gln Gly Gly Gln Leu Gly Ser
100 105 110

Leu Glu Pro Gln Ala Leu Leu Gly Leu Glu Asn Leu Cys His Leu His
115 120 125

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Leu Glu Arg Asn Gln Leu Arg Ser Leu Ala Val Gly Thr Phe Ala Tyr
 130 135 140
 Thr Pro Ala Leu Ala Leu Leu Gly Leu Ser Asn Asn Arg Leu Ser Arg
 145 150 155 160
 Leu Glu Asp Gly Leu Phe Glu Gly Leu Gly Asn Leu Trp Asp Leu Asn
 165 170 175
 Leu Gly Trp Asn Ser Leu Ala Val Leu Pro Asp Ala Ala Phe Arg Gly
 180 185 190
 Leu Gly Gly Leu Arg Glu Leu Val Leu Ala Gly Asn Arg Leu Ala Tyr
 195 200 205
 Leu Gln Pro Ala Leu Phe Ser Gly Leu Ala Glu Leu Arg Glu Leu Asp
 210 215 220
 Leu Ser Arg Asn Ala Leu Arg Ala Ile Lys Ala Asn Val Phe Ala Gln
 225 230 235 240
 Leu Pro Arg Leu Gln Lys Leu Tyr Leu Asp Arg Asn Leu Ile Ala Ala
 245 250 255
 Val Ala Pro Gly Ala Phe Leu Gly Leu Lys Ala Leu Arg Trp Leu Asp
 260 265 270
 Leu Ser His Asn Arg Val Ala Gly Leu Leu Glu Asp Thr Phe Pro Gly
 275 280 285
 Leu Leu Gly Leu Arg Val Leu Arg Leu Ser His Asn Ala Ile Ala Ser
 290 295 300
 Leu Arg Pro Arg Thr Phe Glu Asp Leu His Phe Leu Glu Glu Leu Gln
 305 310 315 320
 Leu Gly His Asn Arg Ile Arg Gln Leu Ala Glu Arg Ser Phe Glu Gly
 325 330 335
 Leu Gly Gln Leu Glu Val Leu Thr Leu Asp His Asn Gln Leu Gln Glu
 340 345 350
 Val Lys Val Gly Ala Phe Leu Gly Leu Thr Asn Val Ala Val Met Asn
 355 360 365
 Leu Ser Gly Asn Cys Leu Arg Asn Leu Pro Glu Gln Val Phe Arg Gly
 370 375 380
 Leu Gly Lys Leu His Ser Leu His Leu Glu Gly Ser Cys Leu Gly Arg
 385 390 395 400
 Ile Arg Pro His Thr Phe Ala Gly Leu Ser Gly Leu Arg Arg Leu Phe
 405 410 415
 Leu Lys Asp Asn Gly Leu Val Gly Ile Glu Glu Gln Ser Leu Trp Gly
 420 425 430
 Leu Ala Glu Leu Leu Glu Leu Asp Leu Thr Ser Asn Gln Leu Thr His
 435 440 445

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<210> 63
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaas at positions 1, 3-4, 6, 8-9, 11, 14, 15 may
be any amino acid

<220>
<223> Xaas at positions 2, 5, 7, 13, 17 and 22 may be
Leu, Ile, Val, Met, Ala, Phe or Tyr

<220>
<223> Xaa at position 10 may be Asn, Cys or Thr

<220>
<223> Xaas at positions 12, 16, 18-21, if present, may
be any amino acid

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 63
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1          5                                10
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Xaa Xaa Xaa Xaa Xaa Xaa
20

<210> 64
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaas at positions 2-7, 9-15, 17-28 and 32-45, if present, may be any amino acid

<220>
<223> Xaa at position 30 may be any amino acid

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 64
Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45

<210> 65
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaas at positions 2-5, 7-11, 13-18, 24 and 26-33 may be any amino acid

<220>
<223> Xaas at positions 19-22 and 24-37, if present, may be any amino acid

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 65
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Cys
35

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<210> 66
 <211> 73
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Consensus
 sequence

<400> 66
 Pro Ser Pro Pro Arg Asn Leu Arg Val Thr Asp Ile Thr Pro Thr Ser
 1 5 10 15
 Ile Thr Val Ser Trp Thr Pro Pro Glu Gly Asn Gly Pro Ile Thr Gly
 20 25 30
 Tyr Arg Ile Gln Tyr Arg Trp Pro Val Asn Asp Asn Glu Trp Asn Glu
 35 40 45
 Phe Asn Val Pro Arg Thr Thr Asn Ser Tyr Thr Ile Thr Asn Leu Arg
 50 55 60
 Pro Gly Thr Glu Tyr Glu Phe Arg Val
 65 70

<210> 67
 <211> 2815
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (197)..(2215)

<400> 67
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 aaggactgag gcccactga ggccttgga cgcaccgcct ggctccttca gccgcagtcg 180
 tctcctggga cagaag atg cac tcc agg agc tgc ctg cca cct ctc ctg ttg 232
 Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu
 1 5 10
 ttg ctt ctg gtg ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc 280
 Leu Leu Leu Val Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly
 15 20 25
 tgc cag tgc aac cag cca cag aca gtc ttc tgc act gcc cgt cag gga 328
 Cys Gln Cys Asn Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly
 30 35 40
 acc aca gtg ccc cga gac gtg cca cct gac aca gtg ggc ctg tac atc 376
 Thr Thr Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile
 45 50 55 60

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ttt gag aac ggc atc acg aca ctt gat gtg ggc tct ttt gct ggc ctt	424
Phe Glu Asn Gly Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu	
65 70 75	
ccg ggc ctg cag ctt ctg gac ttg tca cag aac cag atc act agc ctg	472
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu	
80 85 90	
ccc ggg ggc atc ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg	520
Pro Gly Gly Ile Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu	
95 100 105	
act gcc aac aaa ctg cac gag atc tcc aac gag acc ttc cgt ggc ctg	568
Thr Ala Asn Lys Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu	
110 115 120	
cgg cgc ctg gag cgc ctc tac ctg ggc aag aac cga att cgc cac atc	616
Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile	
125 130 135 140	
caa ccg ggt gcc ttc gac gcg ctt gat cgc ctc ctg gag ctc aag ctg	664
Gln Pro Gly Ala Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu	
145 150 155	
cca gac aat gag ctt cgg gtg ttg ccc cca ttg cac ttg ccc cgc ctg	712
Pro Asp Asn Glu Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu	
160 165 170	
ctg ctg ctt gac ctc agc cac aac agc atc cca gcc ctg gaa gcc gga	760
Leu Leu Leu Asp Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly	
175 180 185	
ata ctg gat acc gcc aat gta gag gca ttg agg ttg gct ggc cta ggg	808
Ile Leu Asp Thr Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly	
190 195 200	
ctg cgg cag ctg gat gag ggg ctt ttt ggc cgc ctt ctc aac ctc cat	856
Leu Arg Gln Leu Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His	
205 210 215 220	
gac ttg gat gtt tct gac aac cag ttg gag cat atg cca tct gtg att	904
Asp Leu Asp Val Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile	
225 230 235	
caa ggc ctg cgt ggc ctg aca cgc ctg cgg ctg gct ggc aac acc cgt	952
Gln Gly Leu Arg Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg	
240 245 250	
att gcc cag ata cgg ccc gag gac ctc gct ggt ctg act gcc cta cag	1000
Ile Ala Gln Ile Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln	
255 260 265	
gaa ttg gat gtg agc aac cta agc ctg cag gcc ctg ccc agt gac ctc	1048
Glu Leu Asp Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu	
270 275 280	
tcg agt ctc ttt ccc cgc ctg cgc ctc tta gca gct gcc agg aac ccc	1096
Ser Ser Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro	
285 290 295 300	

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ttc aac tgc ttg tgc ccc ttg agc tgg ttt ggt cct tgg gtg cgt gag	1144
Phe Asn Cys Leu Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu	
305 310 315	
aac cat gtt gtg ttg gcc agc cct gag gag acg cgt tgt cac ttt cca	1192
Asn His Val Val Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro	
320 325 330	
ccc aag aat gct ggc cga ctg ctc ctg gat ctg gat tat gca gat ttt	1240
Pro Lys Asn Ala Gly Arg Leu Leu Asp Leu Asp Tyr Ala Asp Phe	
335 340 345	
ggc tgc cca gtc acc act acc acg gcc aca gta cct act ata agg tct	1288
Gly Cys Pro Val Thr Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser	
350 355 360	
act atc agg gaa ccc aca ctt tca act tct agc caa gct ccc acc tgg	1336
Thr Ile Arg Glu Pro Thr Leu Ser Thr Ser Ser Gln Ala Pro Thr Trp	
365 370 375 380	
ccc agc ctc aca gag cca act acc cag gcc tcc acc gta cta tcg act	1384
Pro Ser Leu Thr Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr	
385 390 395	
gcc cca cca acc atg agg cca gct cct cag ccc cag gac tgt cca gca	1432
Ala Pro Pro Thr Met Arg Pro Ala Pro Gln Pro Gln Asp Cys Pro Ala	
400 405 410	
tcc atc tgc ctg aat ggt ggt agc tgc cgt ttg gga gca aga cac cac	1480
Ser Ile Cys Leu Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His	
415 420 425	
tgg gag tgc cta tgc cct gag ggc ttc att ggc ctg tac tgt gag agt	1528
Trp Glu Cys Leu Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser	
430 435 440	
cca gtg gag caa ggg atg aag ccc agc tcc ata cca gac act cca agg	1576
Pro Val Glu Gln Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg	
445 450 455 460	
ccc cct cca ctg ctg cct ctc agc att gag ccg gtg agc ccc acc tcc	1624
Pro Pro Pro Leu Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser	
465 470 475	
ttg cgt gtg aag ctg cag cgc tac ttg cag ggt aac act gtg cag cta	1672
Leu Arg Val Lys Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu	
480 485 490	
cgg agc ctc cgg ctc acc tat cgc aac ctg tct ggc cct gac aaa cga	1720
Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg	
495 500 505	
ctg gtg aca tta cgg ctg cct gct tca ctt gca gag tat aca gtc acc	1768
Leu Val Thr Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr	
510 515 520	
cag ctg cga ccc aat gcc acc tat tct atc tgt gtc aca ccc ttg gga	1816
Gln Leu Arg Pro Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly	
525 530 535 540	

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gct gga cgg aca cct gaa ggt gag gag gcc tgt ggg gag gcc aac act	1864
Ala Gly Arg Thr Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala Asn Thr	
545 550 555	
tcc cag gca gtc cgc tct aac cat gcc cca gtt acc cag gcc cgt gag	1912
Ser Gln Ala Val Arg Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu	
560 565 570	
ggc aac ctg cca ctc ctc att gcg cct gcc ctg gct gct gta ctt ctg	1960
Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Val Leu Leu	
575 580 585	
gct gtg tta gcc gct gca ggg gca gcc tac tgt gtg cgg cgg gca cgg	2008
Ala Val Leu Ala Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg	
590 595 600	
gca act tct aca gct cag gac aaa ggg cag gtg ggg cca ggg act gga	2056
Ala Thr Ser Thr Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly	
605 610 615 620	
ccc ctg gaa cta gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag	2104
Pro Leu Glu Leu Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys	
625 630 635	
gca aca gag gga ggt ggg gag gct ttg tca ggt ggt cct gaa tgt gag	2152
Ala Thr Glu Gly Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu	
640 645 650	
gtg cct ctt atg ggc tac cca ggg ccc agc ctt cag ggg gtc ctc cct	2200
Val Pro Leu Met Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro	
655 660 665	
gct aag cac tac att tagactggtg agaaagagca gccaggggggt caggctttca	2255
Ala Lys His Tyr Ile	
670	
gtcaccaccc tctgctgcc acagaaggaa gttctcagta tacaccacag tgcacgtgca	2315
tgatggagct gtgggacct ctctgggctg ggtctcatct gtaagctgct acagcccaga	2375
tgaactctgc cagccgccag tgcattccagt acagcgccctg ccatcttctg caatgtgcaa	2435
ccctgggatg tgagccctgc catgtgctgg taacatggct aggcattgtg ggcttcccaa	2495
accatggagt ctggtaacca gtgaagggaag cccccagaaa taatgagtgg ggaaggtact	2555
agggcactgg ccttggcctc aaaagtgcag gcacacttga aactggaaaag gaaggtgctc	2615
tgggcacatg tggatttgct tctattgttt tgttttgttt tttctaattg atttataaaa	2675
gatcttttcc catttatgct gggaaagtgt ttttcaaact cagtgacaag gactttggtt	2735
tttgtaagac tgttgatgat atgaaggcct tttgtaagaa aataaaaaat aaagtaaaaa	2795
aaaaaaaaa gggcggccgc	2815

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<210> 68
 <211> 673
 <212> PRT
 <213> Mus musculus

<400> 68

Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu Leu Leu Val
 1 5 10 15

Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Asn
 20 25 30

Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro
 35 40 45

Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile Phe Glu Asn Gly
 50 55 60

Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu Pro Gly Leu Gln
 65 70 75 80

Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu Pro Gly Gly Ile
 85 90 95

Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Lys
 100 105 110

Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu
 115 120 125

Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala
 130 135 140

Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu Pro Asp Asn Glu
 145 150 155 160

Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu Leu Leu Leu Asp
 165 170 175

Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly Ile Leu Asp Thr
 180 185 190

Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Arg Gln Leu
 195 200 205

Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His Asp Leu Asp Val
 210 215 220

Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile Gln Gly Leu Arg
 225 230 235 240

Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Ile
 245 250 255

Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln Glu Leu Asp Val
 260 265 270

Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu Ser Ser Leu Phe
 275 280 285

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Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Leu
290 295 300

Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Asn His Val Val
305 310 315 320

Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala
325 330 335

Gly Arg Leu Leu Leu Asp Leu Asp Tyr Ala Asp Phe Gly Cys Pro Val
340 345 350

Thr Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser Thr Ile Arg Glu
355 360 365

Pro Thr Leu Ser Thr Ser Ser Gln Ala Pro Thr Trp Pro Ser Leu Thr
370 375 380

Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr Ala Pro Pro Thr
385 390 395 400

Met Arg Pro Ala Pro Gln Pro Gln Asp Cys Pro Ala Ser Ile Cys Leu
405 410 415

Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His Trp Glu Cys Leu
420 425 430

Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser Pro Val Glu Gln
435 440 445

Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg Pro Pro Pro Leu
450 455 460

Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Lys
465 470 475 480

Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu Arg Ser Leu Arg
485 490 495

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu
500 505 510

Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro
515 520 525

Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly Ala Gly Arg Thr
530 535 540

Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala Asn Thr Ser Gln Ala Val
545 550 555 560

Arg Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro
565 570 575

Leu Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Val Leu Ala
580 585 590

Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg Ala Thr Ser Thr
595 600 605

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Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu
610 615 620

Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly
625 630 635 640

Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met
645 650 655

Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro Ala Lys His Tyr
660 665 670

Ile

<210> 69

<211> 2022

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(2019)

<400> 69

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ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc tgc cag tgc aac 96
Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Asn
20 25 30

cag cca cag aca gtc ttc tgc act gcc cgt cag gga acc aca gtg ccc 144
Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro
35 40 45

cga gac gtg cca cct gac aca gtg ggc ctg tac atc ttt gag aac ggc 192
Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile Phe Glu Asn Gly
50 55 60

atc acg aca ctt gat gtg ggc tgt ttt gct ggc ctt ccg ggc ctg cag 240
Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu Pro Gly Leu Gln
65 70 75 80

ctt ctg gac ttg tca cag aac cag atc act agc ctg ccc ggg ggc atc 288
Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu Pro Gly Gly Ile
85 90 95

ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg act gcc aac aaa 336
Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Lys
100 105 110

ctg cac gag atc tcc aac gag acc ttc cgt ggc ctg cgg cgc ctg gag 384
Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu
115 120 125

- 86 -

cgc ctc tac ctg ggc aag aac cga att cgc cac atc caa ccg ggt gcc	432
Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala	
130 135 140	
ttc gac gcg ctt gat cgc ctc ctg gag ctc aag ctg cca gac aat gag	480
Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu Pro Asp Asn Glu	
145 150 155 160	
ctt cgg gtg ttg ccc cca ttg cac ttg ccc cgc ctg ctg ctg ctt gac	528
Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu Leu Leu Leu Asp	
165 170 175	
ctc agc cac aac agc atc cca gcc ctg gaa gcc gga ata ctg gat acc	576
Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly Ile Leu Asp Thr	
180 185 190	
gcc aat gta gag gca ttg agg ttg gct ggc cta ggg ctg cgg cag ctg	624
Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Arg Gln Leu	
195 200 205	
gat gag ggg ctt ttt ggc cgc ctt ctc aac ctc cat gac ttg gat gtt	672
Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His Asp Leu Asp Val	
210 215 220	
tct gac aac cag ttg gag cat atg cca tct gtg att caa ggc ctg cgt	720
Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile Gln Gly Leu Arg	
225 230 235 240	
ggc ctg aca cgc ctg cgg ctg gct ggc aac acc cgt att gcc cag ata	768
Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Ile	
245 250 255	
cgg ccc gag gac ctc gct ggt ctg act gcc cta cag gaa ttg gat gtg	816
Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln Glu Leu Asp Val	
260 265 270	
agc aac cta agc ctg cag gcc ctg ccc agt gac ctc tcg agt ctc ttt	864
Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu Ser Ser Leu Phe	
275 280 285	
ccc cgc ctg cgc ctc tta gca gct gcc agg aac ccc ttc aac tgc ttg	912
Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Leu	
290 295 300	
tgc ccc ttg agc tgg ttt ggt cct tgg gtg cgt gag aac cat gtt gtg	960
Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Asn His Val Val	
305 310 315 320	
ttg gcc agc cct gag gag acg cgt tgt cac ttt cca ccc aag aat gct	1008
Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala	
325 330 335	
ggc cga ctg ctc ctg gat ctg gat tat gca gat ttt ggc tgc cca gtc	1056
Gly Arg Leu Leu Leu Asp Leu Asp Tyr Ala Asp Phe Gly Cys Pro Val	
340 345 350	
acc act acc acg gcc aca gta cct act ata agg tct act atc agg gaa	1104
Thr Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser Thr Ile Arg Glu	
355 360 365	

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ccc	aca	ctt	tca	act	tct	agc	caa	gct	ccc	acc	tgg	ccc	agc	ctc	aca	1152
Pro	Thr	Leu	Ser	Thr	Ser	Ser	Gln	Ala	Pro	Thr	Trp	Pro	Ser	Leu	Thr	
	370						375				380					
gag	cca	act	acc	cag	gcc	tcc	acc	gta	cta	tgc	act	gcc	cca	cca	acc	1200
Glu	Pro	Thr	Thr	Gln	Ala	Ser	Thr	Val	Leu	Ser	Thr	Ala	Pro	Pro	Thr	
385					390					395					400	
atg	agg	cca	gct	cct	cag	ccc	cag	gac	tgt	cca	gca	tcc	atc	tgc	ctg	1248
Met	Arg	Pro	Ala	Pro	Gln	Pro	Gln	Asp	Cys	Pro	Ala	Ser	Ile	Cys	Leu	
				405					410					415		
aat	ggt	ggt	agc	tgc	cgt	ttg	gga	gca	aga	cac	cac	tgg	gag	tgc	cta	1296
Asn	Gly	Gly	Ser	Cys	Arg	Leu	Gly	Ala	Arg	His	His	Trp	Glu	Cys	Leu	
			420					425					430			
tgc	cct	gag	ggc	ttc	att	ggc	ctg	tac	tgt	gag	agt	cca	gtg	gag	caa	1344
Cys	Pro	Glu	Gly	Phe	Ile	Gly	Leu	Tyr	Cys	Glu	Ser	Pro	Val	Glu	Gln	
		435					440					445				
ggg	atg	aag	ccc	agc	tcc	ata	cca	gac	act	cca	agg	ccc	cct	cca	ctg	1392
Gly	Met	Lys	Pro	Ser	Ser	Ile	Pro	Asp	Thr	Pro	Arg	Pro	Pro	Pro	Leu	
	450					455					460					
ctg	cct	ctc	agc	att	gag	ccg	gtg	agc	ccc	acc	tcc	ttg	cgt	gtg	aag	1440
Leu	Pro	Leu	Ser	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Lys	
465					470					475					480	
ctg	cag	cgc	tac	ttg	cag	ggt	aac	act	gtg	cag	cta	cgg	agc	ctc	cgg	1488
Leu	Gln	Arg	Tyr	Leu	Gln	Gly	Asn	Thr	Val	Gln	Leu	Arg	Ser	Leu	Arg	
				485					490					495		
ctc	acc	tat	cgc	aac	ctg	tct	ggc	cct	gac	aaa	cga	ctg	gtg	aca	tta	1536
Leu	Thr	Tyr	Arg	Asn	Leu	Ser	Gly	Pro	Asp	Lys	Arg	Leu	Val	Thr	Leu	
			500					505					510			
cgg	ctg	cct	gct	tca	ctt	gca	gag	tat	aca	gtc	acc	cag	ctg	cga	ccc	1584
Arg	Leu	Pro	Ala	Ser	Leu	Ala	Glu	Tyr	Thr	Val	Thr	Gln	Leu	Arg	Pro	
		515					520					525				
aat	gcc	acc	tat	tct	atc	tgt	gtc	aca	ccc	ttg	gga	gct	gga	cgg	aca	1632
Asn	Ala	Thr	Tyr	Ser	Ile	Cys	Val	Thr	Pro	Leu	Gly	Ala	Gly	Arg	Thr	
	530					535					540					
cct	gaa	ggt	gag	gag	gcc	tgt	ggg	gag	gcc	aac	act	tcc	cag	gca	gtc	1680
Pro	Glu	Gly	Glu	Glu	Ala	Cys	Gly	Glu	Ala	Asn	Thr	Ser	Gln	Ala	Val	
545					550					555					560	
cgc	tct	aac	cat	gcc	cca	ggt	acc	cag	gcc	cgt	gag	ggc	aac	ctg	cca	1728
Arg	Ser	Asn	His	Ala	Pro	Val	Thr	Gln	Ala	Arg	Glu	Gly	Asn	Leu	Pro	
				565					570					575		
ctc	ctc	att	gcg	cct	gcc	ctg	gct	gct	gta	ctt	ctg	gct	gtg	tta	gcc	1776
Leu	Leu	Ile	Ala	Pro	Ala	Leu	Ala	Ala	Val	Leu	Leu	Ala	Val	Leu	Ala	
			580					585					590			
gct	gca	ggg	gca	gcc	tac	tgt	gtg	cgg	cgg	gca	cgg	gca	act	tct	aca	1824
Ala	Ala	Gly	Ala	Ala	Tyr	Cys	Val	Arg	Arg	Ala	Arg	Ala	Thr	Ser	Thr	
		595					600					605				

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gct cag gac aaa ggg cag gtg ggg cca ggg act gja ccc ctg gaa cta 1872
 Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu
 610 615 620

gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag gca aca gag gga 1920
 Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly
 625 630 635 640

ggt ggg gag gct ttg tca ggt ggt cct gaa tgt gag gtg cct ctt atg 1968
 Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met
 645 650 655

ggc tac cca ggg ccc agc ctt cag ggg gtc ctc cct gct aag cac tac 2016
 Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro Ala Lys His Tyr
 660 665 670

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 <213> Homo sapiens

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 cggagcgcgc cggccgcggg tggccgccc cagcatgccc cggcccgcgg gccgctccgc 180
 cgccagccac ccccgcggcc ctccgcggcc tgcgctcggc ccgggggccc gggaaccgca 240
 gccggagccg gaggcgggag cagcgagccg gagccccggg cgctcgaatg caggatgctc 300
 gtggtcccca gcacacctga gccaccagga gtgagggctg ctgctccctg agacctggt 360
 ccaaggagga tgccacagcc gcctgccagc tccggtctgc acc atg agt gat gag 415
 Met Ser Asp Glu
 1

cgg cgg ctg cct ggc agt gca gtg ggc tgg ctg gta tgt ggg ggc ctc 463
 Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val Cys Gly Gly Leu
 5 10 15 20

tcc ctg ctg gcc aat gcc tgg ggc atc ctc agc gtt ggc gcc aag cag 511
 Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln
 25 30 35

aag aag tgg aag ccc ttg gag ttc ctg ctg tgt acg ctc gcg gcc acc 559
 Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr
 40 45 50

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cac atg cta aat ctg gcc gtg ccc atc gcc acc tac tcc gtg gtg cag	607
His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln	
55 60 65	
ctg cgg cgg cag cgc ccc gac ttc gag tgg aat gag ggt ctc tgc aag	655
Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys	
70 75 80	
gtc ttc gtg tcc acc ttc tac acc ctc acc ctg gcc acc tgt ttc tct	703
Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser	
85 90 95 100	
gtc acc tcc ctc tcc tac cac cgc atg tgg atg gtc tgc tgg cct gtc	751
Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val	
105 110 115	
aac tac cgg ctg agc aat gcc aag aag cag gcg gtg cac aca gtc atg	799
Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met	
120 125 130	
ggg atc tgg atg gtg tcc ttc atc ctg tcg gcc ctg cct gcc gtt ggc	847
Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly	
135 140 145	
tgg cac gac acc agc gag cgc ttc tac acc cat ggc tgc cgc ttc atc	895
Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile	
150 155 160	
gtg gct gag atc ggc ctg ggc ttt ggc gtc tgc ttc ctg ctg ctg gtg	943
Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val	
165 170 175 180	
ggc ggc agc gtg gcc atg ggc gtg atc tgc aca gcc atc gcc ctc ttc	991
Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala Ile Ala Leu Phe	
185 190 195	
cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac cac cgc gcc ttc	1039
Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp His Arg Ala Phe	
200 205 210	
acc gtg ccc acc atc gtg gtg gag gac gcg cag ggc aag cgg cgc tcc	1087
Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly Lys Arg Arg Ser	
215 220 225	
tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg cag acc acg ggc	1135
Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu Gln Thr Thr Gly	
230 235 240	
ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc atg ggc ttc cct	1183
Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu Met Gly Phe Pro	
245 250 255 260	
gtg ctg gac tct acg ccc atc ccc gaa agg tct gca gtg aga cag gga	1231
Val Leu Asp Ser Thr Pro Ile Pro Glu Arg Ser Ala Val Arg Gln Gly	
265 270 275	
gag gac tgg ggc aaa gac cag cct gag ggg ttt cat cca agc agc agg	1279
Glu Asp Trp Gly Lys Asp Gln Pro Glu Gly Phe His Pro Ser Ser Arg	
280 285 290	

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caa gac tgc ctt ccc tgagccattg caggacatga ggacatgagc tccagaatgg 1334
 Gln Asp Cys Leu Pro
 295

tgccaggccg agccctgtgc ccacaggtgg tgagcttcag cagcctgcgg gccgacgcct 1394
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 <212> PRT
 <213> Homo sapiens

<400> 71

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 Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val
 20 25 30
 Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr
 35 40 45
 Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr
 50 55 60
 Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu
 65 70 75 80
 Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala
 85 90 95
 Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val
 100 105 110
 Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val
 115 120 125
 His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu
 130 135 140
 Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly
 145 150 155 160
 Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe
 165 170 175
 Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala
 180 185 190
 Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp
 195 200 205
 His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly
 210 215 220
 Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu
 225 230 235 240
 Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu
 245 250 255
 Met Gly Phe Pro Val Leu Asp Ser Thr Pro Ile Pro Glu Arg Ser Ala
 260 265 270
 Val Arg Gln Gly Glu Asp Trp Gly Lys Asp Gln Pro Glu Gly Phe His
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Pro Ser Ser Arg Gln Asp Cys Leu Pro
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Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val
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tgt ggg ggc ctc tcc ctg ctg gcc aat gcc tgg ggc atc ctc agc gtt 96
Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val
20 25 30
ggc gcc aag cag aag aag tgg aag ccc ttg gag ttc ctg ctg tgt acg 144
Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr
35 40 45
ctc gcg gcc acc cac atg cta aat gtg gcc gtg ccc atc gcc acc tac 192
Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr
50 55 60
tcc gtg gtg cag ctg cgg cgg cag cgc ccc gac ttc gag tgg aat gag 240
Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu
65 70 75 80
ggt ctc tgc aag gtc ttc gtg tcc acc ttc tac acc ctc acc ctg gcc 288
Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala
85 90 95
acc tgt ttc tct gtc acc tcc ctc tcc tac cac cgc atg tgg atg gtc 336
Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val
100 105 110
tgc tgg cct gtc aac tac cgg ctg agc aat gcc aag aag cag gcg gtg 384
Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val
115 120 125
cac aca gtc atg ggt atc tgg atg gtg tcc ttc atc ctg tcg gcc ctg 432
His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu
130 135 140
cct gcc gtt ggc tgg cac gac acc agc gag cgc ttc tac acc cat ggc 480
Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly
145 150 155 160
tgc cgc ttc atc gtg gct gag atc ggc ctg ggc ttt ggc gtc tgc ttc 528
Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe
165 170 175

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ctg ctg ctg gtg ggc ggc agc gtg gcc atg ggc gtg atc tgc aca gcc 576
 Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala
 180 185 190

atc gcc ctc ttc cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac 624
 Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp
 195 200 205

cac cgc gcc ttc acc gtg ccc acc atc gtg gtg gag gac gcg cag ggc 672
 His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly
 210 215 220

aag cgg cgc tcc tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg 720
 Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu
 225 230 235 240

cag acc acg ggc ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc 768
 Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu
 245 250 255

atg ggc ttc cct gtg ctg gac tct acg ccc atc ccc gaa agg tct gca 816
 Met Gly Phe Pro Val Leu Asp Ser Thr Pro Ile Pro Glu Arg Ser Ala
 260 265 270

gtg aga cag gga gag gac tgg ggc aaa gac cag cct gag ggg ttt cat 864
 Val Arg Gln Gly Glu Asp Trp Gly Lys Asp Gln Pro Glu Gly Phe His
 275 280 285

cca agc agc agg caa gac tgc ctt ccc 891
 Pro Ser Ser Arg Gln Asp Cys Leu Pro
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 ccccgcgggc ctcggcgggc tgcgctcggc ccgggggccc gggaaccgca gccggagccg 180
 gaggcgggag cagcgagccg gagccccggg cgctcgaatg caggatgctc gtggtcccca 240
 gcaccccttga gccaccagga gtgagggctg ctgctccctg agacctggct ccaaggagga 300
 tgccacagcc gcctgccagc tccggtctgc acc atg agt gat gag cgg cgg ctg 354
 Met Ser Asp Glu Arg Arg Leu
 1 5

cct ggc agt gca gtg ggc tgg ctg gta tgt ggg ggc ctc tcc ctg ctg 402
 Pro Gly Ser Ala Val Gly Trp Leu Val Cys Gly Gly Leu Ser Leu Leu
 10 15 20

- 94 -

gcc aat gcc tgg ggc atc ctc agc gtt ggc gcc aag cag aag aag tgg	450
Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln Lys Lys Trp	
25 30 35	
aag ccc ttg gag ttc ctg ctg tgt acg ctc gcg gcc acc cac atg cta	498
Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr His Met Leu	
40 45 50 55	
aat gtg gcc gtg ccc atc gcc acc tac tcc gtg gtg cag ctg cgg cgg	546
Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln Leu Arg Arg	
60 65 70	
cag cgc ccc gac ttc gag tgg aat gag ggt ctc tgc aag gtc ttc gtg	594
Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys Val Phe Val	
75 80 85	
tcc acc ttc tac acc ctc acc ctg gcc acc tgt ttc tct gtc acc tcc	642
Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser Val Thr Ser	
90 95 100	
ctc tcc tac cac cgc atg tgg atg gtc tgc tgg cct gtc aac tac cgg	690
Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val Asn Tyr Arg	
105 110 115	
ctg agc aat gcc aag aag cag gcg gtg cac aca gtc atg ggt atc tgg	738
Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met Gly Ile Trp	
120 125 130 135	
atg gtg tcc ttc atc ctg tgc gcc ctg cct gcc gtt ggc tgg cac gac	786
Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly Trp His Asp	
140 145 150	
acc agc gag cgc ttc tac acc cat gcc tgc cgc ttc atc gtg gct gag	834
Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile Val Ala Glu	
155 160 165	
atc gcc ctg ggc ttt ggc gtc tgc ttc ctg ctg ctg gtg ggc ggc agc	882
Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val Gly Gly Ser	
170 175 180	
gtg gcc atg ggc gtg atc tgc aca gcc atc gcc ctc ttc cag acg ctg	930
Val Ala Met Gly Val Ile Cys Thr Ala Ile Ala Leu Phe Gln Thr Leu	
185 190 195	
gcc gtg cag gtg ggg cgc cag gcc gac cac cgc gcc ttc acc gtg ccc	978
Ala Val Gln Val Gly Arg Gln Ala Asp His Arg Ala Phe Thr Val Pro	
200 205 210 215	
acc atc gtg gtg gag gac gcg cag gcc aag cgg cgc tcc tcc atc gat	1026
Thr Ile Val Val Glu Asp Ala Gln Gly Lys Arg Arg Ser Ser Ile Asp	
220 225 230	
ggc tgc gag ccc gcc aaa acc tct ctg cag acc acg ggc ctc gtg acc	1074
Gly Ser Glu Pro Ala Lys Thr Ser Leu Gln Thr Thr Gly Leu Val Thr	
235 240 245	
acc ata gtc ttc atc tac gac tgc ctc atg gcc ttc cct gtg ctg gtg	1122
Thr Ile Val Phe Ile Tyr Asp Cys Leu Met Gly Phe Pro Val Leu Val	
250 255 260	

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gtg agc ttc agc agc ctg cgg gcc gac gcc tca gcg ccc tgg atg gca Val Ser Phe Ser Ser Leu Arg Ala Asp Ala Ser Ala Pro Trp Met Ala 265 270 275	1170
ctc tgc gtg ctg tgg tgc tcc gtg gcc cag gcc ctg ctg ctg cct gtg Leu Cys Val Leu Trp Cys Ser Val Ala Gln Ala Leu Leu Leu Pro Val 280 285 290 295	1218
ttc ctc tgg gcc tgc gac cgc tac cgg gct gac ctc aaa gct gtc cgg Phe Leu Trp Ala Cys Asp Arg Tyr Arg Ala Asp Leu Lys Ala Val Arg 300 305 310	1266
gag aag tgc atg gcc ctc atg gcc aac gac gag gag tca gac gat gag Glu Lys Cys Met Ala Leu Met Ala Asn Asp Glu Glu Ser Asp Asp Glu 315 320 325	1314
acc agc ctg gaa ggt ggc atc tcc ccg gac ctg gtg ttg gag cgc tcc Thr Ser Leu Glu Gly Gly Ile Ser Pro Asp Leu Val Leu Glu Arg Ser 330 335 340	1362
ctg gac tat ggc tat gga ggt gat ttt gtg gcc cta gat agg atg gcc Leu Asp Tyr Gly Tyr Gly Gly Asp Phe Val Ala Leu Asp Arg Met Ala 345 350 355	1410
aag tat gag atc tcc gcc ctg gag ggg ggc ctg ccc cag ctc tac cca Lys Tyr Glu Ile Ser Ala Leu Glu Gly Gly Leu Pro Gln Leu Tyr Pro 360 365 370 375	1458
ctg cgg ccc ttg cag gag gac aag atg caa tac ctg cag gtc ccg ccc Leu Arg Pro Leu Gln Glu Asp Lys Met Gln Tyr Leu Gln Val Pro Pro 380 385 390	1506
acg cgg cgc ttc tcc cac gac gat gcg gac gtg tgg gcc gcc gtc ccg Thr Arg Arg Phe Ser His Asp Asp Ala Asp Val Trp Ala Ala Val Pro 395 400 405	1554
ctg ccc gcc ttc ctg ccg cgc tgg ggc tcc ggc gag gac ctg gcc gcc Leu Pro Ala Phe Leu Pro Arg Trp Gly Ser Gly Glu Asp Leu Ala Ala 410 415 420	1602
ctg gcg cac ctg gtg ctg cct gcc ggg ccc gag cgg cgc cgc gcc agc Leu Ala His Leu Val Leu Pro Ala Gly Pro Glu Arg Arg Arg Ala Ser 425 430 435	1650
ctc ctg gcc ttc gcg gag gac gca cca ccg tcc cgc gcg cgc cgc cgc Leu Leu Ala Phe Ala Glu Asp Ala Pro Pro Ser Arg Ala Arg Arg Arg 440 445 450 455	1698
tcg gcc gag agc ctg ctg tcg ctg cgg acc tcg gcc ctg gat agc ggc Ser Ala Glu Ser Leu Leu Ser Leu Arg Thr Ser Ala Leu Asp Ser Gly 460 465 470	1746
ccg cgg gga gcc cgc gac tcg ccc ccc ggc agc ccg cgc cgc cgc ccc Pro Arg Gly Ala Arg Asp Ser Pro Pro Gly Ser Pro Arg Arg Arg Pro 475 480 485	1794
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gcc ctg acc gcc ttc gag tgc gag cca cag gcc ctg cgc cgc ccg ccc 1890
 Ala Leu Thr Ala Phe Glu Cys Glu Pro Gln Ala Leu Arg Arg Pro Pro
 505 510 515

ggg ccc ttc ccc gct gcg ccc gcc gcc ccc gac ggc gca gat ccc gga 1938
 Gly Pro Phe Pro Ala Ala Pro Ala Ala Pro Asp Gly Ala Asp Pro Gly
 520 525 530 535

gag gcc ccg acg ccc cca agc agc gcc cag cgg agc cca ggg cca cgc 1986
 Glu Ala Pro Thr Pro Pro Ser Ser Ala Gln Arg Ser Pro Gly Pro Arg
 540 545 550

ccc tct gcg cac tcg cac gcc ggc tct ctg cgc ccc ggc ctg agc gcg 2034
 Pro Ser Ala His Ser His Ala Gly Ser Leu Arg Pro Gly Leu Ser Ala
 555 560 565

tcg tgg ggc gag ccc ggg ggg ctg cgc gcg gcg ggc ggc ggc ggc agc 2082
 Ser Trp Gly Glu Pro Gly Gly Leu Arg Ala Ala Gly Gly Gly Gly Ser
 570 575 580

acc agc agc ttc ctg agt tcc ccc tcc gag tcc tcg ggc tac gcc acg 2130
 Thr Ser Ser Phe Leu Ser Ser Pro Ser Glu Ser Ser Gly Tyr Ala Thr
 585 590 595

ctg cac tcg gac tcg ctg ggc tcc gcg tcc taggaccgcc ggcgcctccc 2180
 Leu His Ser Asp Ser Leu Gly Ser Ala Ser
 600 605

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cccccgcgc gcagacatgc gccaccctc ccaggggtga gggggcgttg gcctcagcgt 2300

ttgtcttcg gctcctccca gctggccttg tcccaggggc gacggctgcc ccggacgact 2360

gcgctgggca ccgcatgtcc cgggccgagt gaggtcgggc ctggggagct gagtgcacac 2420

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aggcctccca ctctcagtgc cccctgcccc cttgggaacc cacactccac cccagctaag 2960

cacaacactg tggaccacca ccaatggcac ctgagccacc ttgaccacca ttagtgtccc 3020

caccctcatt actctgccgt cgttgccctg cccaccaca tcctctccct ccatggctcc 3080

caccatgacg ctggcaggtg caagcggaga gcacgagggc agcagggcct ggccttccgt 3140

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gtccctgcgt catccccagc ctcaactcccc acccgtgcag gcctggccag gaagggatcc 3200
tggcaggggc ttccaggttc tcagctcaag gcctgggtccc gggcaggcgt ccaacccttg 3260
ggagcaatgt atttctttgc cttccatcct gggcagaccc cttacaggcc tgggcattgc 3320
catgggccct gggctcttccc aggctaagga gaaccaggaa cagctataac cttgagctag 3380
tgaaataggg tagatgagaa ggctgtctcc tccagacccc taccctaca cagtggcccc 3440
acaatatgaa gacctggggt aattccaagg tgagcataga gcctgcctgt gccagttcc 3500
ttctggccct caggtggcca agcccatctc ttcatccttc agatagggtc cactcccag 3560
aagaagctgc tgggggtggg gtgggaggct gcctaagcct gtctgtgctt cagaggcccc 3620
tccagtcctt ggctgtgggg taactggggg tatgagctgt ggccacaggc gagcaaggca 3680
gggaactgca atccagccct ggccgcggga ggggccatct ctggccaatg ctgctgtgcc 3740
ttcaaggact gacaagttac gtaggggcag aggtcgccag ctagccagtg tctcctccat 3800
ctggggggcg tctgtccact tgtcacctta ggttttctact catttgtcac cttggggttt 3860
tgctctgtgt gtttcatatc caacggcaat acttgcaggg ggacagagtc ctctaaatac 3920
tccaatcctg cggtttttac aaacataaag ggggagaccc caagtggagg accctggggc 3980
tggagctccc tcccaaactt tgtccagcat ccagcctgtt ccctgggctc actggggagg 4040
gagttgtctt catagcacac ccagagccag ggatcccttt gtagtttttt gacaacggag 4100
catttctctt ctgtacagga cccaataaaa acttccttat gaaaaaaaaa aaaaaagggc 4160
ggccgc

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4166

<210> 74
 <211> 609
 <212> PRT
 <213> Homo sapiens

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<400> 74
Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val
 1             5             10            15
Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val
      20             25            30
Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr
      35             40            45
Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr
      50             55            60
Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu
      65             70            75            80

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Gly	Leu	Cys	Lys	Val	Phe	Val	Ser	Thr	Phe	Tyr	Thr	Leu	Thr	Leu	Ala	85	90	95
Thr	Cys	Phe	Ser	Val	Thr	Ser	Leu	Ser	Tyr	His	Arg	Met	Trp	Met	Val	100	105	110
Cys	Trp	Pro	Val	Asn	Tyr	Arg	Leu	Ser	Asn	Ala	Lys	Lys	Gln	Ala	Val	115	120	125
His	Thr	Val	Met	Gly	Ile	Trp	Met	Val	Ser	Phe	Ile	Leu	Ser	Ala	Leu	130	135	140
Pro	Ala	Val	Gly	Trp	His	Asp	Thr	Ser	Glu	Arg	Phe	Tyr	Thr	His	Gly	145	150	155
Cys	Arg	Phe	Ile	Val	Ala	Glu	Ile	Gly	Leu	Gly	Phe	Gly	Val	Cys	Phe	165	170	175
Leu	Leu	Leu	Val	Gly	Gly	Ser	Val	Ala	Met	Gly	Val	Ile	Cys	Thr	Ala	180	185	190
Ile	Ala	Leu	Phe	Gln	Thr	Leu	Ala	Val	Gln	Val	Gly	Arg	Gln	Ala	Asp	195	200	205
His	Arg	Ala	Phe	Thr	Val	Pro	Thr	Ile	Val	Val	Glu	Asp	Ala	Gln	Gly	210	215	220
Lys	Arg	Arg	Ser	Ser	Ile	Asp	Gly	Ser	Glu	Pro	Ala	Lys	Thr	Ser	Leu	225	230	235
Gln	Thr	Thr	Gly	Leu	Val	Thr	Thr	Ile	Val	Phe	Ile	Tyr	Asp	Cys	Leu	245	250	255
Met	Gly	Phe	Pro	Val	Leu	Val	Val	Ser	Phe	Ser	Ser	Leu	Arg	Ala	Asp	260	265	270
Ala	Ser	Ala	Pro	Trp	Met	Ala	Leu	Cys	Val	Leu	Trp	Cys	Ser	Val	Ala	275	280	285
Gln	Ala	Leu	Leu	Leu	Pro	Val	Phe	Leu	Trp	Ala	Cys	Asp	Arg	Tyr	Arg	290	295	300
Ala	Asp	Leu	Lys	Ala	Val	Arg	Glu	Lys	Cys	Met	Ala	Leu	Met	Ala	Asn	305	310	315
Asp	Glu	Glu	Ser	Asp	Asp	Glu	Thr	Ser	Leu	Glu	Gly	Gly	Ile	Ser	Pro	325	330	335
Asp	Leu	Val	Leu	Glu	Arg	Ser	Leu	Asp	Tyr	Gly	Tyr	Gly	Gly	Asp	Phe	340	345	350
Val	Ala	Leu	Asp	Arg	Met	Ala	Lys	Tyr	Glu	Ile	Ser	Ala	Leu	Glu	Gly	355	360	365
Gly	Leu	Pro	Gln	Leu	Tyr	Pro	Leu	Arg	Pro	Leu	Gln	Glu	Asp	Lys	Met	370	375	380
Gln	Tyr	Leu	Gln	Val	Pro	Pro	Thr	Arg	Arg	Phe	Ser	His	Asp	Asp	Ala	385	390	395

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Asp Val Trp Ala Ala Val Pro Leu Pro Ala Phe Leu Pro Arg Trp Gly
405 410 415

Ser Gly Glu Asp Leu Ala Ala Leu Ala His Leu Val Leu Pro Ala Gly
420 425 430

Pro Glu Arg Arg Arg Ala Ser Leu Leu Ala Phe Ala Glu Asp Ala Pro
435 440 445

Pro Ser Arg Ala Arg Arg Arg Ser Ala Glu Ser Leu Leu Ser Leu Arg
450 455 460

Thr Ser Ala Leu Asp Ser Gly Pro Arg Gly Ala Arg Asp Ser Pro Pro
465 470 475 480

Gly Ser Pro Arg Arg Arg Pro Gly Pro Gly Pro Arg Ser Ala Ser Ala
485 490 495

Ser Leu Leu Pro Asp Ala Phe Ala Leu Thr Ala Phe Glu Cys Glu Pro
500 505 510

Gln Ala Leu Arg Arg Pro Pro Gly Pro Phe Pro Ala Ala Pro Ala Ala
515 520 525

Pro Asp Gly Ala Asp Pro Gly Glu Ala Pro Thr Pro Pro Ser Ser Ala
530 535 540

Gln Arg Ser Pro Gly Pro Arg Pro Ser Ala His Ser His Ala Gly Ser
545 550 555 560

Leu Arg Pro Gly Leu Ser Ala Ser Trp Gly Glu Pro Gly Gly Leu Arg
565 570 575

Ala Ala Gly Gly Gly Gly Ser Thr Ser Ser Phe Leu Ser Ser Pro Ser
580 585 590

Glu Ser Ser Gly Tyr Ala Thr Leu His Ser Asp Ser Leu Gly Ser Ala
595 600 605

Ser

<210> 75
<211> 1827
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1827)

<400> 75
atg agt gat gag cgg cgg ctg cct ggc agt gca gtg ggc tgg ctg gta 48
Met Ser Asp Glu Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val
1 5 10 15

tgt ggg ggc ctc tcc ctg ctg gcc aat gcc tgg ggc atc ctc agc gtt 96
Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val
20 25 30

- 100 -

ggc gcc aag cag aag aag tgg aag ccc ttg gag ttc ctg ctg tgt acg	144
Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr	
35 40 45	
ctc gcg gcc acc cac atg cta aat gtg gcc gtg ccc atc gcc acc tac	192
Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr	
50 55 60	
tcc gtg gtg cag ctg cgg cgg cag cgc ccc gac ttc gag tgg aat gag	240
Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu	
65 70 75 80	
ggt ctc tgc aag gtc ttc gtg tcc acc ttc tac acc ctc acc ctg gcc	288
Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala	
85 90 95	
acc tgt ttc tct gtc acc tcc ctc tcc tac cac cgc atg tgg atg gtc	336
Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val	
100 105 110	
tgc tgg cct gtc aac tac cgg ctg agc aat gcc aag aag cag gcg gtg	384
Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val	
115 120 125	
cac aca gtc atg ggt atc tgg atg gtg tcc ttc atc ctg tcg gcc ctg	432
His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu	
130 135 140	
cct gcc gtt ggc tgg cac gac acc agc gag cgc ttc tac acc cat ggc	480
Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly	
145 150 155 160	
tgc cgc ttc atc gtg gct gag atc ggc ctg ggc ttt ggc gtc tgc ttc	528
Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe	
165 170 175	
ctg ctg ctg gtg ggc ggc agc gtg gcc atg ggc gtg atc tgc aca gcc	576
Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala	
180 185 190	
atc gcc ctc ttc cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac	624
Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp	
195 200 205	
cac cgc gcc ttc acc gtg ccc acc atc gtg gtg gag gac gcg cag ggc	672
His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly	
210 215 220	
aag cgg cgc tcc tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg	720
Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu	
225 230 235 240	
cag acc acg ggc ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc	768
Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu	
245 250 255	
atg ggc ttc cct gtg ctg gtg gtg agc ttc agc agc ctg cgg gcc gac	816
Met Gly Phe Pro Val Leu Val Val Ser Phe Ser Ser Leu Arg Ala Asp	
260 265 270	

- 101 -

gcc tca gcg ccc tgg atg gca ctc tgc gtg ctg tgg tgc tcc gtg gcc	864
Ala Ser Ala Pro Trp Met Ala Leu Cys Val Leu Trp Cys Ser Val Ala	
275 280 285	
cag gcc ctg ctg ctg cct gtg ttc ctc tgg gcc tgc gac cgc tac cgg	912
Gln Ala Leu Leu Leu Pro Val Phe Leu Trp Ala Cys Asp Arg Tyr Arg	
290 295 300	
gct gac ctc aaa gct gtc cgg gag aag tgc atg gcc ctc atg gcc aac	960
Ala Asp Leu Lys Ala Val Arg Glu Lys Cys Met Ala Leu Met Ala Asn	
305 310 315 320	
gac gag gag tca gac gat gag acc agc ctg gaa ggt ggc atc tcc ccg	1008
Asp Glu Glu Ser Asp Asp Glu Thr Ser Leu Glu Gly Gly Ile Ser Pro	
325 330 335	
gac ctg gtg ttg gag cgc tcc ctg gac tat ggc tat gga ggt gat ttt	1056
Asp Leu Val Leu Glu Arg Ser Leu Asp Tyr Gly Tyr Gly Gly Asp Phe	
340 345 350	
gtg gcc cta gat agg atg gcc aag tat gag atc tcc gcc ctg gag ggg	1104
Val Ala Leu Asp Arg Met Ala Lys Tyr Glu Ile Ser Ala Leu Glu Gly	
355 360 365	
ggc ctg ccc cag ctc tac cca ctg cgg ccc ttg cag gag gac aag atg	1152
Gly Leu Pro Gln Leu Tyr Pro Leu Arg Pro Leu Gln Glu Asp Lys Met	
370 375 380	
caa tac ctg cag gtc ccg ccc acg cgg cgc ttc tcc cac gac gat gcg	1200
Gln Tyr Leu Gln Val Pro Pro Thr Arg Arg Phe Ser His Asp Asp Ala	
385 390 395 400	
gac gtg tgg gcc gcc gtc ccg ctg ccc gcc ttc ctg ccg cgc tgg ggc	1248
Asp Val Trp Ala Ala Val Pro Leu Pro Ala Phe Leu Pro Arg Trp Gly	
405 410 415	
tcc ggc gag gac ctg gcc gcc ctg gcg cac ctg gtg ctg cct gcc ggg	1296
Ser Gly Glu Asp Leu Ala Ala Leu Ala His Leu Val Leu Pro Ala Gly	
420 425 430	
ccc gag cgg cgc cgc gcc agc ctc ctg gcc ttc gcg gag gac gca cca	1344
Pro Glu Arg Arg Arg Ala Ser Leu Leu Ala Phe Ala Glu Asp Ala Pro	
435 440 445	
ccg tcc cgc gcg cgc cgc cgc tcg gcc gag agc ctg ctg tcg ctg cgg	1392
Pro Ser Arg Ala Arg Arg Arg Ser Ala Glu Ser Leu Leu Ser Leu Arg	
450 455 460	
acc tcg gcc ctg gat agc ggc ccg cgg gga gcc cgc gac tcg ccc ccc	1440
Thr Ser Ala Leu Asp Ser Gly Pro Arg Gly Ala Arg Asp Ser Pro Pro	
465 470 475 480	
ggc agc ccg cgc cgc cgc ccc ggg ccc ggc ccc cgc tcc gcc tcg gcc	1488
Gly Ser Pro Arg Arg Arg Pro Gly Pro Gly Pro Arg Ser Ala Ser Ala	
485 490 495	
tcg ctg ctg ccc gac gcc ttc gcc ctg acc gcc ttc gag tgc gag cca	1536
Ser Leu Leu Pro Asp Ala Phe Ala Leu Thr Ala Phe Glu Cys Glu Pro	
500 505 510	

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cag gcc ctg cgc cgc ccg ccc ggg ccc ttc ccc gct gcg ccc gcc gcc 1584
Gln Ala Leu Arg Arg Pro Pro Gly Pro Phe Pro Ala Ala Pro Ala Ala
515 520 525

ccc gac ggc gca gat ccc gga gag gcc ccg acg ccc cca agc agc gcc 1632
Pro Asp Gly Ala Asp Pro Gly Glu Ala Pro Thr Pro Pro Ser-Ser Ala
530 535 540

cag cgg agc cca ggg cca cgc ccc tct gcg cac tcg cac gcc ggc tct 1680
Gln Arg Ser Pro Gly Pro Arg Pro Ser Ala His Ser His Ala Gly Ser
545 550 555 560

ctg cgc ccc ggc ctg agc gcg tcg tgg ggc gag ccc ggg ggg ctg cgc 1728
Leu Arg Pro Gly Leu Ser Ala Ser Trp Gly Glu Pro Gly Gly Leu Arg
565 570 575

gcg gcg ggc ggc ggc ggc agc acc agc agc ttc ctg agt tcc ccc tcc 1776
Ala Ala Gly Gly Gly Gly Ser Thr Ser Ser Phe Leu Ser Ser Pro Ser
580 585 590

gag tcc tcg ggc tac gcc acg ctg cac tcg gac tcg ctg ggc tcc gcg 1824
Glu Ser Ser Gly Tyr Ala Thr Leu His Ser Asp Ser Leu Gly Ser Ala
595 600 605

tcc 1827
Ser

<210> 76
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<223> Xaas at positions 38, 55 and 56 may be any amino
acid

<400> 76
Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
1 5 10 15
Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
20 25 30
Phe Ser Leu Phe Thr Xaa Met Pro Phe Trp Met Val Tyr Tyr Val Met
35 40 45
Gln Gly Arg Trp Pro Phe Xaa Xaa Gly Asp Phe Met Cys Arg Ile Trp
50 55 60
Met Tyr Phe Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr
65 70 75 80
Cys Ile Ser Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg
85 90 95
Tyr Met Arg Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile
100 105 110

- 103 -

Ile Ile Trp Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met
 115 120 125
 Phe Arg Trp Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp
 130 135 140
 Cys Met Ile Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile
 145 150 155 160
 Leu Met Thr Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu
 165 170 175

Phe

<210> 77
 <211> 107
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> Xaa at position 84 may be any amino acid

<400> 77
 Ile Gln Glu Arg Met Asn Glu Leu Asn Asp Arg Trp Glu Arg Leu Lys
 1 5 10 15
 Glu Leu Met Glu Gln Arg Arg Gln Met Leu Glu Asp Ser Met Arg Leu
 20 25 30
 Gln Gln Phe Phe Arg Asp Met Asp Glu Glu Glu Ser Trp Ile Asn Glu
 35 40 45
 Lys Glu Gln Ile Leu Asn Ser Asp Asp Tyr Gly Lys Asp Leu Thr Ser
 50 55 60
 Val Gln Asn Leu Leu Lys Lys His Gln Ala Phe Glu Ala Asp Ile Ala
 65 70 75 80
 Ala His Glu Xaa Asp Arg Ile Gln Ala Leu Asn Glu Phe Ala Gln Gln
 85 90 95
 Leu Ile Gln Glu Asn His Tyr Ala Ser Glu Glu
 100 105

<210> 78
 <211> 588
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Ala Arg Gly Gly Ala Gly Ala Glu Glu Ala Ser Leu Arg Ser Asn
 1 5 10 15
 Ala Leu Ser Trp Leu Ala Cys Gly Leu Leu Ala Leu Leu Ala Asn Ala
 20 25 30

- 104 -

Trp Ile Ile Leu Ser Ile Ser Ala Lys Gln Gln Lys His Lys Pro Leu
 35 40 45
 Glu Leu Leu Leu Cys Phe Leu Ala Gly Thr His Ile Leu Met Ala Ala
 50 55 60
 Val Pro Leu Thr Thr Phe Ala Val Val Gln Leu Arg Arg Gln Ala Ser
 65 70 75 80
 Ser Asp Tyr Asp Trp Asn Glu Ser Ile Cys Lys Val Phe Val Ser Thr
 85 90 95
 Tyr Tyr Thr Leu Ala Leu Ala Thr Cys Phe Thr Val Ala Ser Leu Ser
 100 105 110
 Tyr His Arg Met Trp Met Val Arg Trp Pro Val Asn Tyr Arg Leu Ser
 115 120 125
 Asn Ala Lys Lys Gln Ala Leu His Ala Val Met Gly Ile Trp Met Val
 130 135 140
 Ser Phe Ile Leu Ser Thr Leu Pro Ser Ile Gly Trp His Asn Asn Gly
 145 150 155 160
 Glu Arg Tyr Tyr Ala Arg Gly Cys Gln Phe Ile Val Ser Lys Ile Gly
 165 170 175
 Leu Gly Phe Gly Val Cys Phe Ser Leu Leu Leu Leu Gly Gly Ile Val
 180 185 190
 Met Gly Leu Val Cys Val Ala Ile Thr Phe Tyr Gln Thr Leu Trp Ala
 195 200 205
 Arg Pro Arg Arg Ala Arg Gln Ala Arg Arg Val Gly Gly Gly Gly Gly
 210 215 220
 Thr Lys Ala Gly Gly Pro Gly Ala Leu Gly Thr Arg Pro Ala Phe Glu
 225 230 235 240
 Val Pro Ala Ile Val Val Glu Asp Ala Arg Gly Lys Arg Arg Ser Ser
 245 250 255
 Leu Asp Gly Ser Glu Ser Ala Lys Thr Ser Leu Gln Val Thr Asn Leu
 260 265 270
 Val Ser Ala Ile Val Phe Leu Tyr Asp Ser Leu Thr Gly Val Pro Ile
 275 280 285
 Leu Val Val Ser Phe Phe Ser Leu Lys Ser Asp Ser Ala Pro Pro Trp
 290 295 300
 Met Val Leu Ala Val Leu Trp Cys Ser Met Ala Gln Thr Leu Leu Leu
 305 310 315 320
 Pro Ser Phe Ile Trp Ser Cys Glu Arg Tyr Arg Ala Asp Val Arg Thr
 325 330 335
 Val Trp Glu Gln Cys Val Ala Ile Met Ser Glu Glu Asp Gly Asp Asp
 340 345 350

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Asp Gly Gly Cys Asp Asp Tyr Ala Glu Gly Arg Val Cys Lys Val Arg
 355 360 365
 Phe Asp Ala Asn Gly Ala Thr Gly Pro Gly Ser Arg Asp Pro Ala Gln
 370 375 380
 Val Lys Leu Leu Pro Gly Arg His Met Leu Phe Pro Pro Leu Glu Arg
 385 390 395 400
 Val His Tyr Leu Gln Val Pro Leu Ser Arg Arg Leu Ser His Asp Glu
 405 410 415
 Thr Asn Ile Phe Ser Thr Pro Arg Glu Pro Gly Ser Phe Leu His Lys
 420 425 430
 Trp Ser Ser Ser Asp Asp Ile Arg Val Leu Pro Ala Gln Ser Arg Ala
 435 440 445
 Leu Gly Gly Pro Pro Glu Tyr Leu Gly Gln Arg His Arg Leu Glu Asp
 450 455 460
 Glu Glu Asp Glu Glu Glu Ala Glu Gly Gly Gly Leu Ala Ser Leu Arg
 465 470 475 480
 Gln Phe Leu Glu Ser Gly Val Leu Gly Ser Gly Gly Gly Pro Pro Arg
 485 490 495
 Gly Pro Gly Phe Phe Arg Glu Glu Ile Thr Thr Phe Ile Asp Glu Thr
 500 505 510
 Pro Leu Pro Ser Pro Thr Ala Ser Pro Gly His Ser Pro Arg Arg Pro
 515 520 525
 Arg Pro Leu Gly Leu Ser Pro Arg Arg Leu Ser Leu Gly Ser Pro Glu
 530 535 540
 Ser Arg Ala Val Gly Leu Pro Leu Gly Leu Ser Ala Gly Arg Arg Cys
 545 550 555 560
 Ser Leu Thr Gly Gly Glu Glu Ser Ala Arg Ala Trp Gly Gly Ser Trp
 565 570 575
 Gly Pro Gly Asn Pro Ile Phe Pro Gln Leu Thr Leu
 580 585

<210> 79

<211> 227

<212> PRT

<213> Homo sapiens

<400> 79

Ile Thr Phe Tyr Gln Thr Leu Trp Ala Arg Pro Arg Arg Ala Arg Gln
 1 5 10 15

Ala Arg Arg Val Gly Gly Gly Gly Gly Thr Lys Ala Gly Gly Pro Gly
 20 25 30

Ala Leu Gly Thr Arg Pro Ala Phe Glu Val Pro Ala Ile Val Val Glu
 35 40 45

- 106 -

Asp Ala Arg Gly Lys Arg Arg Ser Ser Leu Asp Gly Ser Glu Ser Ala
50 55 60

Lys Thr Ser Leu Gln Val Thr Asn Leu Val Val Ser Phe Phe Ser Leu
65 70 75 80

Lys Ser Asp Ser Ala Pro Pro Trp Met Val Leu Ala Val Leu Trp Cys
85 90 95

Ser Met Ala Gln Thr Leu Leu Leu Pro Ser Phe Ile Trp Ser Cys Glu
100 105 110

Arg Tyr Arg Ala Asp Val Arg Thr Val Trp Glu Gln Cys Val Ala Ile
115 120 125

Met Ser Glu Glu Asp Gly Asp Asp Asp Gly Gly Cys Asp Asp Tyr Ala
130 135 140

Glu Gly Arg Val Cys Lys Val Arg Phe Asp Ala Asn Gly Ala Thr Gly
145 150 155 160

Pro Gly Ser Arg Asp Pro Ala Gln Val Lys Leu Leu Pro Gly Arg His
165 170 175

Met Leu Phe Pro Pro Leu Glu Arg Val His Tyr Leu Gln Leu Lys Lys
180 185 190

Leu Asp Leu Ala Ala Ala Ala Ala His Thr Phe Phe Val Ala Asn Pro
195 200 205

Met His Leu Gln Met Arg Glu Asp Met Ala Lys Tyr Arg Arg Met Ser
210 215 220

Gly Val Arg
225

<210> 80
<211> 425
<212> PRT
<213> Homo sapiens

<400> 80
Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
1 5 10 15

Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
20 25 30

Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
35 40 45

Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
50 55 60

Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
65 70 75 80

Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu		
				85					90								
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val		
			100				105								110		
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile		
		115					120								125		
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu		
		130					135								140		
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser		
		145					150								155	160	
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg		
			165							170						175	
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu		
		180							185						190		
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met		
		195							200						205		
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu		
		210					215								220		
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys		
		225					230								235	240	
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp		
			245							250						255	
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser		
		260							265						270		
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val		
		275							280						285		
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn		
		290					295								300		
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys		
		305					310								315	320	
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His		
			325							330						335	
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala		
		340							345						350		
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro		
		355							360						365		
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser		
		370							375						380		
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser		
		385							390						395	400	

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Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
 405 410 415

Asn Ser Ile Tyr Lys Lys Leu Leu Thr
 420 425

<210> 81
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 81
 Met Asn Gly Thr Glu Gly Pro Asn Phe Tyr Val Pro Phe Ser Asn Ala
 1 5 10 15

Thr Gly Val Val Arg Ser Pro Phe Glu Tyr Pro Gln Tyr Tyr Leu Ala
 20 25 30

Glu Pro Trp Gln Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile
 35 40 45

Val Leu Gly Phe Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln
 50 55 60

His Lys Lys Leu Arg Thr Pro Leu Asn Tyr Ile Leu Leu Asn Leu Ala
 65 70 75 80

Val Ala Asp Leu Phe Met Val Leu Gly Gly Phe Thr Ser Thr Leu Tyr
 85 90 95

Thr Ser Leu His Gly Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu
 100 105 110

Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu
 115 120 125

Val Val Leu Ala Ile Glu Arg Tyr Val Val Val Cys Lys Pro Met Ser
 130 135 140

Asn Phe Arg Phe Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr
 145 150 155 160

Trp Val Met Ala Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp Ser
 165 170 175

Arg Tyr Ile Pro Glu Gly Leu Gln Cys Ser Cys Gly Ile Asp Tyr Tyr
 180 185 190

Thr Leu Lys Pro Glu Val Asn Asn Glu Ser Phe Val Ile Tyr Met Phe
 195 200 205

Val Val His Phe Thr Ile Pro Met Ile Ile Ile Phe Phe Cys Tyr Gly
 210 215 220

Gln Leu Val Phe Thr Val Lys Glu Ala Ala Ala Gln Gln Gln Glu Ser
 225 230 235 240

Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Ile Ile
 245 250 255

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Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro Tyr Ala Ser Val Ala
 260 265 270

Phe Tyr Ile Phe Thr His Gln Gly Ser Asn Phe Gly Pro Ile Phe Met
 275 280 285

Thr Ile Pro Ala Phe Phe Ala Lys Ser Ala Ala Ile Tyr Asn Pro Val
 290 295 300

Ile Tyr Ile Met Met Asn Lys Gln Phe Arg Asn Cys Met Leu Thr Thr
 305 310 315 320

Ile Cys Cys Gly Lys Asn Pro Leu Gly Asp Asp Glu Ala Ser Ala Thr
 325 330 335

Val Ser Lys Thr Glu Thr Ser Gln Val Ala Pro Ala
 340 345

<210> 82
 <211> 460
 <212> PRT
 <213> Rattus Norvegicus

<400> 82
 Met Asn Thr Ser Val Pro Pro Ala Val Ser Pro Asn Ile Thr Val Leu
 1 5 10 15

Ala Pro Gly Lys Gly Pro Trp Gln Val Ala Phe Ile Gly Ile Thr Thr
 20 25 30

Gly Leu Leu Ser Leu Ala Thr Val Thr Gly Asn Leu Leu Val Leu Ile
 35 40 45

Ser Phe Lys Val Asn Thr Glu Leu Lys Thr Val Asn Asn Tyr Phe Leu
 50 55 60

Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr Phe Ser Met Asn
 65 70 75 80

Leu Tyr Thr Thr Tyr Leu Leu Met Gly His Trp Ala Leu Gly Thr Leu
 85 90 95

Ala Cys Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser
 100 105 110

Val Met Asn Leu Leu Leu Ile Ser Phe Asp Arg Tyr Phe Ser Val Thr
 115 120 125

Arg Pro Leu Ser Tyr Arg Ala Lys Arg Thr Pro Arg Arg Ala Ala Leu
 130 135 140

Met Ile Gly Leu Ala Trp Leu Val Ser Phe Val Leu Trp Ala Pro Ala
 145 150 155 160

Ile Leu Phe Trp Gln Tyr Leu Val Gly Glu Arg Thr Val Leu Ala Gly
 165 170 175

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Gln Cys Tyr Ile Gln Phe Leu Ser Gln Pro Ile Ile Thr Phe Gly Thr
180 185 190

Ala Met Ala Ala Phe Tyr Leu Pro Val Thr Val Met Cys Thr Leu Tyr
195 200 205

Trp Arg Ile Tyr Arg Glu Thr Glu Asn Arg Ala Arg Glu Leu Ala Ala
210 215 220

Leu Gln Gly Ser Glu Thr Pro Gly Lys Gly Gly Gly Ser Ser Ser Ser
225 230 235 240

Ser Glu Arg Ser Gln Pro Gly Ala Glu Gly Ser Pro Glu Ser Pro Pro
245 250 255

Gly Arg Cys Cys Arg Cys Cys Arg Ala Pro Arg Leu Leu Gln Ala Tyr
260 265 270

Ser Trp Lys Glu Glu Glu Glu Glu Asp Glu Gly Ser Met Glu Ser Leu
275 280 285

Thr Ser Ser Glu Gly Glu Glu Pro Gly Ser Glu Val Val Ile Lys Met
290 295 300

Pro Met Val Asp Ser Glu Ala Gln Ala Pro Thr Lys Gln Pro Pro Lys
305 310 315 320

Ser Ser Pro Asn Thr Val Lys Arg Pro Thr Lys Lys Gly Arg Asp Arg
325 330 335

Gly Gly Lys Gly Gln Lys Pro Arg Gly Lys Glu Gln Leu Ala Lys Arg
340 345 350

Lys Thr Phe Ser Leu Val Lys Glu Lys Lys Ala Ala Arg Thr Leu Ser
355 360 365

Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro Tyr Asn Ile Met
370 375 380

Val Leu Val Ser Thr Phe Cys Lys Asp Cys Val Pro Glu Thr Leu Trp
385 390 395 400

Glu Leu Gly Tyr Trp Leu Cys Tyr Val Asn Ser Thr Val Asn Pro Met
405 410 415

Cys Tyr Ala Leu Cys Asn Lys Ala Phe Arg Asp Thr Phe Arg Leu Leu
420 425 430

Leu Leu Cys Arg Trp Asp Lys Arg Arg Trp Arg Lys Ile Pro Lys Arg
435 440 445

Pro Gly Ser Val His Arg Thr Pro Ser Arg Gln Cys
450 455 460

<210> 83
<211> 350
<212> PRT
<213> Homo sapiens

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<400> 83

Met	Ser	Asn	Ile	Thr	Asp	Pro	Gln	Met	Trp	Asp	Phe	Asp	Asp	Leu	Asn	1	5	10	15
Phe	Thr	Gly	Met	Pro	Pro	Ala	Asp	Glu	Asp	Tyr	Ser	Pro	Cys	Met	Leu	20	25	30	
Glu	Thr	Glu	Thr	Leu	Asn	Lys	Tyr	Val	Val	Ile	Ile	Ala	Tyr	Ala	Leu	35	40	45	
Val	Phe	Leu	Leu	Ser	Leu	Leu	Gly	Asn	Ser	Leu	Val	Met	Leu	Val	Ile	50	55	60	
Leu	Tyr	Ser	Arg	Val	Gly	Arg	Ser	Val	Thr	Asp	Val	Tyr	Leu	Leu	Asn	65	70	75	80
Leu	Ala	Leu	Ala	Asp	Leu	Leu	Phe	Ala	Leu	Thr	Leu	Pro	Ile	Trp	Ala	85	90	95	
Ala	Ser	Lys	Val	Asn	Gly	Trp	Ile	Phe	Gly	Thr	Phe	Leu	Cys	Lys	Val	100	105	110	
Val	Ser	Leu	Leu	Lys	Glu	Val	Asn	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu	115	120	125	
Ala	Cys	Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Thr	Arg	130	135	140	
Thr	Leu	Thr	Gln	Lys	Arg	His	Leu	Val	Lys	Phe	Val	Cys	Leu	Gly	Cys	145	150	155	160
Trp	Gly	Leu	Ser	Met	Asn	Leu	Ser	Leu	Pro	Phe	Phe	Leu	Phe	Arg	Gln	165	170	175	
Ala	Tyr	His	Pro	Asn	Asn	Ser	Ser	Pro	Val	Cys	Tyr	Glu	Val	Leu	Gly	180	185	190	
Asn	Asp	Thr	Ala	Lys	Trp	Arg	Met	Val	Leu	Arg	Ile	Leu	Pro	His	Thr	195	200	205	
Phe	Gly	Phe	Ile	Val	Pro	Leu	Phe	Val	Met	Leu	Phe	Cys	Tyr	Gly	Phe	210	215	220	
Thr	Leu	Arg	Thr	Leu	Phe	Lys	Ala	His	Met	Gly	Gln	Lys	His	Arg	Ala	225	230	235	240
Met	Arg	Val	Ile	Phe	Ala	Val	Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu	245	250	255	
Pro	Tyr	Asn	Leu	Val	Leu	Leu	Ala	Asp	Thr	Leu	Met	Arg	Thr	Gln	Val	260	265	270	
Ile	Gln	Glu	Thr	Cys	Glu	Arg	Arg	Asn	Asn	Ile	Gly	Arg	Ala	Leu	Asp	275	280	285	
Ala	Thr	Glu	Ile	Leu	Gly	Phe	Leu	His	Ser	Cys	Leu	Asn	Pro	Ile	Ile	290	295	300	
Tyr	Ala	Phe	Ile	Gly	Gln	Asn	Phe	Arg	His	Gly	Phe	Leu	Lys	Ile	Leu	305	310	315	320

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Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val
 325 330 335

Thr Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu
 340 345 350

<210> 84

<211> 601

<212> PRT

<213> *Drosophila melanogaster*

<400> 84

Met Pro Ser Ala Asp Gln Ile Leu Phe Val Asn Val Thr Thr Thr Val
 1 5 10 15

Ala Ala Ala Ala Leu Thr Ala Ala Ala Val Ser Thr Thr Lys Ser
 20 25 30

Gly Asn Gly Asn Ala Ala Arg Gly Tyr Thr Asp Ser Asp Asp Ala
 35 40 45

Gly Met Gly Thr Glu Ala Val Ala Asn Ile Ser Gly Ser Leu Val Glu
 50 55 60

Gly Leu Thr Thr Val Thr Ala Ala Leu Ser Thr Ala Gln Ala Asp Lys
 65 70 75 80

Asp Ser Ala Gly Glu Cys Glu Gly Ala Val Glu Glu Leu His Ala Ser
 85 90 95

Ile Leu Gly Leu Gln Leu Ala Val Pro Glu Trp Glu Ala Leu Leu Thr
 100 105 110

Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile Ile Gly Asn Ile
 115 120 125

Leu Val Ile Leu Ser Val Phe Thr Tyr Lys Pro Leu Arg Ile Val Gln
 130 135 140

Asn Phe Phe Ile Val Ser Leu Ala Val Ala Asp Leu Thr Val Ala Leu
 145 150 155 160

Leu Val Leu Pro Phe Asn Val Ala Tyr Ser Ile Leu Gly Arg Trp Glu
 165 170 175

Phe Gly Ile His Leu Cys Lys Leu Trp Leu Thr Cys Asp Val Leu Cys
 180 185 190

Cys Thr Ser Ser Ile Leu Asn Leu Cys Ala Ile Ala Leu Asp Arg Tyr
 195 200 205

Trp Ala Ile Thr Asp Pro Ile Asn Tyr Ala Gln Lys Arg Thr Val Gly
 210 215 220

Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser Leu Leu Ile
 225 230 235 240

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Ser Ser Pro Pro Leu Ile Gly Trp Asn Asp Trp Pro Asp Glu Phe Thr
245 250 255

Ser Ala Thr Pro Cys Glu Leu Thr Ser Gln Arg Gly Tyr Val Ile Tyr
260 265 270

Ser Ser Leu Gly Ser Phe Phe Ile Pro Leu Ala Ile Met Thr Ile Val
275 280 285

Tyr Ile Glu Ile Phe Val Ala Thr Arg Arg Arg Leu Arg Glu Arg Ala
290 295 300

Arg Ala Asn Lys Leu Asn Thr Ile Ala Leu Lys Ser Thr Glu Leu Glu
305 310 315 320

Pro Met Ala Asn Ser Ser Pro Val Ala Ala Ser Asn Ser Gly Ser Lys
325 330 335

Ser Arg Leu Leu Ala Ser Trp Leu Cys Cys Gly Arg Asp Arg Ala Gln
340 345 350

Phe Ala Thr Pro Met Ile Gln Asn Asp Gln Glu Ser Ile Ser Ser Glu
355 360 365

Thr His Gln Pro Gln Asp Ser Ser Lys Ala Gly Pro His Gly Asn Ser
370 375 380

Asp Pro Gln Gln Gln His Val Val Val Leu Val Lys Lys Ser Arg Arg
385 390 395 400

Ala Lys Thr Lys Asp Ser Ile Lys His Gly Lys Thr Arg Gly Gly Arg
405 410 415

Lys Ser Gln Ser Ser Ser Thr Cys Glu Pro His Gly Glu Gln Gln Leu
420 425 430

Leu Pro Ala Gly Gly Asp Gly Gly Ser Cys Gln Pro Gly Gly Gly His
435 440 445

Ser Gly Gly Gly Lys Ser Asp Ala Glu Ile Ser Thr Glu Ser Gly Ser
450 455 460

Asp Pro Lys Gly Cys Ile Gln Val Cys Val Thr Gln Ala Asp Glu Gln
465 470 475 480

Thr Ser Leu Lys Leu Thr Pro Pro Gln Ser Ser Thr Gly Val Ala Ala
485 490 495

Val Ser Val Thr Pro Leu Gln Lys Lys Thr Ser Gly Val Asn Gln Phe
500 505 510

Ile Glu Glu Lys Gln Lys Ile Ser Leu Ser Lys Glu Arg Arg Ala Ala
515 520 525

Arg Thr Leu Gly Ile Ile Met Gly Val Phe Val Ile Cys Trp Leu Pro
530 535 540

Phe Phe Leu Met Tyr Val Ile Leu Pro Phe Cys Gln Thr Cys Cys Pro
545 550 555 560

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Thr Asn Lys Phe Lys Asn Phe Ile Thr Trp Leu Gly Tyr Ile Asn Ser
565 570 575

Gly Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Leu Asp Tyr Arg Arg
580 585 590

Ala Phe Lys Arg Leu Leu Gly Leu Asn
595 600

<210> 85
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
agatgccacc ttccaggct 19

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
ggagaagtgc atggccctc 19

<210> 87
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 87
tctcatcgtc tgactcctcg tcgttgg 27

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 88
ggcgggtgcac acagttat 18

- 115 -

<210> 89
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 89
 agagagcgct ccaaatacca t

21

<210> 90
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 90
 Lys Arg Arg Ser
 1

<210> 91
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 91
 Ser Ser Ile Asp
 1

<210> 92
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 92
 Ser Arg Gln Asp
 1

<210> 93
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 93
 Gly Ser Ala Val Gly Trp
 1 5

<210> 94
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 94
 Gly Leu Gly Phe Gly Val
 1 5

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<210> 95
<211> 6
<212> PRT
<213> Homo sapiens

<400> 95
Gly Gly Ser Val Ala Met
1 5

<210> 96
<211> 6
<212> PRT
<213> Homo sapiens

<400> 96
Gly Val Ile Cys Thr Ala
1 5

<210> 97
<211> 6
<212> PRT
<213> Homo sapiens

<400> 97
Gly Ser Glu Pro Ala Lys
1 5

<210> 98
<211> 6
<212> PRT
<213> Homo sapiens

<400> 98
Gly Leu Val Thr Thr Ile
1 5

<210> 99
<211> 4
<212> PRT
<213> Homo sapiens

<400> 99
Gln Gly Lys Arg
1

<210> 100
<211> 4
<212> PRT
<213> Homo sapiens

<400> 100
Lys Arg Arg Ser
1

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<210> 101
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 101
 Arg Arg Phe Ser
 1

<210> 102
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 102
 Arg Arg Ala Ser
 1

<210> 103
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 103
 Arg Arg Arg Ser
 1

<210> 104
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 104
 Ser Ser Ile Asp
 1

<210> 105
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 105
 Ser Ser Asp Glu
 1

<210> 106
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 106
 Thr Ser Leu Glu
 1

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<210> 107
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 107
 Ser Ala Leu Glu
 1

<210> 108
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 108
 Ser His Asp Asp
 1

<210> 109
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 109
 Ser Gly Glu Asp
 1

<210> 110
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 110
 Ser Ala Leu Asp
 1

<210> 111
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 111
 Thr Ala Phe Glu
 1

<210> 112
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 112
 Ser Trp Gly Glu
 1

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<210> 113
<211> 4
<212> PRT
<213> Homo sapiens

<400> 113
Ser Pro Ser Glu
1

<210> 114
<211> 7
<212> PRT
<213> Homo sapiens

<400> 114
Arg Ser Leu Asp Tyr Gly Tyr
1 5

<210> 115
<211> 6
<212> PRT
<213> Homo sapiens

<400> 115
Gly Ser Ala Val Gly Trp
1 5

<210> 116
<211> 6
<212> PRT
<213> Homo sapiens

<400> 116
Gly Leu Gly Phe Gly Val
1 5

<210> 117
<211> 6
<212> PRT
<213> Homo sapiens

<400> 117
Gly Gly Ser Val Ala Met
1 5

<210> 118
<211> 6
<212> PRT
<213> Homo sapiens

<400> 118
Gly Val Ile Cys Thr Ala
1 5

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<210> 119
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 119
 Gly Ser Glu Pro Ala Lys
 1 5

<210> 120
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 120
 Gly Leu Val Thr Thr Ile
 1 5

<210> 121
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 121
 Gly Ala Asp Pro Gly Glu
 1 5

<210> 122
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 122
 Gly Leu Ser Ala Ser Trp
 1 5

<210> 123
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 123
 Gly Gly Leu Arg Ala Ala
 1 5

<210> 124
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 124
 Gly Gly Gly Gly Ser Thr
 1 5

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<210> 125
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 125
 Gln Gly Lys Arg
 1

<210> 126
 <211> 458
 <212> PRT
 <213> Mus Musculus

<400> 126
 Met Thr Lys Glu Met Thr Glu Asn Gln Arg Leu Cys Pro His Glu Arg
 1 5 10 15
 Glu Asp Ala Asp Cys Ser Ser Glu Ser Val Lys Phe Asp Ala Arg Ser
 20 25 30
 Met Thr Ala Ser Leu Pro His Ser Thr Lys Asn Gly Pro Ser Val Gln
 35 40 45
 Glu Lys Leu Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu
 50 55 60
 Val Phe Ala Val Leu Ile Pro Val Val Gly Ile Val Thr Ala Gln Leu
 65 70 75 80
 Leu Asn Trp Glu Met Lys Asn Cys Leu Val Cys Ser Arg Asn Thr Ser
 85 90 95
 Asp Thr Ser Gln Gly Pro Met Glu Lys Glu Asn Thr Ser Asn Val Glu
 100 105 110
 Met Arg Phe Thr Ile Ile Met Ala His Met Lys Asp Met Glu Glu Arg
 115 120 125
 Ile Gln Ser Ile Ser Asn Ser Lys Ala Asp Leu Ile Asp Thr Gly Arg
 130 135 140
 Phe Gln Asn Phe Ser Met Ala Thr Asp Gln Arg Leu Asn Asp Ile Leu
 145 150 155 160
 Leu Gln Leu Asn Ser Leu Ile Leu Ser Val Gln Glu His Gly Asn Ser
 165 170 175
 Leu Asp Ala Ile Ser Lys Ser Leu Gln Ser Leu Asn Met Thr Leu Leu
 180 185 190
 Asp Val Gln Leu His Thr Glu Thr Leu His Val Arg Val Arg Glu Ser
 195 200 205
 Thr Ala Lys Gln Gln Glu Asp Ile Ser Lys Leu Glu Glu Arg Val Tyr
 210 215 220

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Lys Val Ser Ala Glu Val Gln Ser Val Lys Glu Glu Gln Ala His Val
 225 230 235 240

Glu Gln Glu Val Lys Gln Glu Val Arg Val Leu Asn Asn Ile Thr Asn
 245 250 255

Asp Leu Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Lys Asn Ile
 260 265 270

Thr Phe Ile Gln Gly Pro Pro Gly Pro Gln Gly Glu Lys Gly Asp Arg
 275 280 285

Gly Leu Thr Gly Gln Thr Gly Pro Pro Gly Ala Pro Gly Ile Arg Gly
 290 295 300

Ile Pro Gly Val Lys Gly Asp Arg Gly Gln Ile Gly Phe Pro Gly Gly
 305 310 315 320

Arg Gly Asn Pro Gly Ala Pro Gly Lys Pro Gly Arg Ser Gly Ser Pro
 325 330 335

Gly Pro Lys Gly Gln Lys Gly Glu Lys Gly Ser Val Gly Gly Ser Thr
 340 345 350

Pro Leu Lys Thr Val Arg Leu Val Gly Gly Ser Gly Ala His Glu Gly
 355 360 365

Arg Val Glu Ile Phe His Gln Gly Gln Trp Gly Thr Ile Cys Asp Asp
 370 375 380

Arg Trp Asp Ile Arg Ala Gly Gln Val Val Cys Arg Ser Leu Gly Tyr
 385 390 395 400

Gln Glu Val Leu Ala Val His Lys Arg Ala His Phe Gly Gln Gly Thr
 405 410 415

Gly Pro Ile Trp Leu Asn Glu Val Met Cys Phe Gly Arg Glu Ser Ser
 420 425 430

Ile Glu Asn Cys Lys Ile Asn Gln Trp Gly Val Leu Ser Cys Ser His
 435 440 445

Ser Glu Asp Ala Gly Val Thr Cys Thr Ser
 450 455

<210> 127

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at position 2 and 4 may be any amino acid
 except Pro

<220>

<223> Xaa at position 3 may be Ser or Thr

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<220>
<223> Description of Artificial Sequence: Amidation
consensus site

<400> 127
Asn Xaa Xaa Xaa
1

<210> 128
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<220>
<223> Xaa at position 2 can be between 4 and 14 amino
acids

<220>
<223> Xaa at position, if present, may be between 0 or 2
amino acids

<220>
<223> Xaa at position 6 may be between 2 and 4 amino
acids

<220>
<223> Xaa at position 8 may be between 6 and 12 amino
acids

<220>
<223> Xaa at position 10 may be between 6 and 10 amino
acids

<400> 128
Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys
1 5 10

<210> 129
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<220>
<223> Xaa at position 2 may be 4 or 6 amino acids

<220>
<223> Xaa at position 6 may be 5 or 10 amino acids

<220>
<223> Xaa at position 8 may be 0 or 2 amino acids

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<220>

<223> Xaa at position 10 may be 7 or 11 amino acids

<220>

<223> Xaa at position 12 may be 4 or 6 amino acids

<400> 129

Cys Xaa Phe Tyr His Xaa Cys Xaa Cys Xaa Cys Xaa Asp Asn Glu Gln
1 5 10 15

Ser Lys Pro Xaa Xaa Cys
20

<210> 130

<211> 39

<212> PRT

<213> Mus musculus

<400> 130

Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys
1 5 10 15

Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly
20 25 30

Tyr Gly Glu Asp Ala Gln Cys
35

<210> 131

<211> 40

<212> PRT

<213> Mus musculus

<400> 131

Cys Arg Pro His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys
1 5 10 15

Pro Cys Ala Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys
20 25 30

Ser His Thr Ser Asp Ala Val Cys
35 40

<210> 132

<211> 39

<212> PRT

<213> Mus musculus

<400> 132

Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys
1 5 10 15

Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly
20 25 30

- 125 -

Tyr Gly Glu Asp Ala Gln Cys
35

<210> 133
<211> 40
<212> PRT
<213> Mus musculus

<400> 133
Cys Arg Pro His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys
1 5 10 15

Pro Cys Ala Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys
20 25 30

Ser His Thr Ser Asp Ala Val Cys
35 40

<210> 134
<211> 29
<212> PRT
<213> Mus musculus

<400> 134
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys
20 25

<210> 135
<211> 29
<212> PRT
<213> Mus musculus

<400> 135
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys
20 25

<210> 136
<211> 25
<212> PRT
<213> Mus musculus

<400> 136
Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr Val Leu Leu Ala
1 5 10 15

Leu Leu Ile Leu Cys Val Ile Tyr Cys
20 25

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<210> 137

<211> 31

<212> PRT

<213> Homo sapiens

<400> 137

Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val Phe Val Val Ser Leu
 1 5 10 15

Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile Leu Lys Met Lys
 20 25 30

<210> 138

<211> 31

<212> PRT

<213> Homo sapiens

<400> 138

Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile Val Leu Gly Phe
 1 5 10 15

Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln His Lys Lys
 20 25 30

<210> 139

<211> 31

<212> PRT

<213> Rattus Norvegicus

<400> 139

Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu Ser Leu Ala Thr Val
 1 5 10 15

Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys Val Asn Thr Glu
 20 25 30

<210> 140

<211> 31

<212> PRT

<213> Homo sapiens

<400> 140

Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu Leu Ser Leu
 1 5 10 15

Leu Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val
 20 25 30

<210> 141

<211> 31

<212> PRT

<213> Drosophila melanogaster

<400> 141

Ala Leu Leu Thr Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile
 1 5 10 15

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<210> 142
<211> 28
<212> PRT
<213> Homo sapiens
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Val Leu Pro Phe Lys Ile Ser Tyr Tyr Phe Ser Gly
20 25

<400> 143
Asn Tyr Ile Leu Leu Asn Leu Ala Val Ala Asp Leu Phe Met Val Leu
1 5 10 15

Gly Gly Phe Thr Ser Thr Leu Tyr Thr Ser Leu His
20 25

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<210> 144
<211> 28
<212> PRT
<213> Rattus Norvegicus
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<400> 144
Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr
1 5 10 15

Phe Ser Met Asn Leu Tyr Thr Thr Tyr Leu Leu Met
20 25

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<210> 145
<211> 28
<212> PRT
<213> Homo sapiens
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<400> 145
Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
1 5 10 15

Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly
20 25

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<210> 146
 <211> 28
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 146
 Asn Phe Phe Ile Val Ser Leu Ala Val Ala Asp Leu Thr Val Ala Leu
 1 5 10 15
 Leu Val Leu Pro Phe Asn Val Ala Tyr Ser Ile Leu
 20 25

<210> 147
 <211> 25
 <212> PRT
 <213> *Homo sapiens*

<400> 147
 Arg Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu
 1 5 10 15
 Leu Met Thr Val Ile Ser Ile Asp Arg
 20 25

<210> 148
 <211> 25
 <212> PRT
 <213> *Homo sapiens*

<400> 148
 Asn Leu Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp
 1 5 10 15
 Ser Leu Val Val Leu Ala Ile Glu Arg
 20 25

<210> 149
 <211> 25
 <212> PRT
 <213> *Rattus Norvegicus*

<400> 149
 Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser Val Met
 1 5 10 15
 Asn Leu Leu Leu Ile Ser Phe Asp Arg
 20 25

<210> 150
 <211> 25
 <212> PRT
 <213> *Homo sapiens*

<400> 150
 Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu
 1 5 10 15

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Leu Leu Ala Cys Ile Ser Val Asp Arg
20 25

<210> 151
<211> 25
<212> PRT
<213> *Drosophila melanogaster*

<400> 151
Lys Leu Trp Leu Thr Cys Asp Val Leu Cys Cys Thr Ser Ser Ile Leu
1 5 10 15

Asn Leu Cys Ala Ile Ala Leu Asp Arg
20 25

<210> 152
<211> 27
<212> PRT
<213> *Homo sapiens*

<400> 152
Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu Ala Ile Trp Ala Leu Ala
1 5 10 15

Ile Ala Gly Val Val Pro Leu Val Leu Lys Glu
20 25

<210> 153
<211> 27
<212> PRT
<213> *Homo sapiens*

<400> 153
Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr Trp Val Met Ala
1 5 10 15

Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp
20 25

<210> 154
<211> 27
<212> PRT
<213> *Rattus Norvegicus*

<400> 154
Thr Pro Arg Arg Ala Ala Leu Met Ile Gly Leu Ala Trp Leu Val Ser
1 5 10 15

Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp
20 25

- 130 -

<210> 155
 <211> 27
 <212> PRT
 <213> Homo sapiens

<400> 155
 Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser
 1 5 10 15
 Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg
 20 25

<210> 156
 <211> 27
 <212> PRT
 <213> Drosophila melanogaster

<400> 156
 Thr Val Gly Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser
 1 5 10 15
 Leu Leu Ile Ser Ser Pro Pro Leu Ile Gly Trp
 20 25

<210> 157
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 157
 Ala Tyr Tyr Phe Ser Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu
 1 5 10 15
 Ile Ile Ser Thr Val Cys Tyr Val Ser Ile Ile Arg Cys
 20 25

<210> 158
 <211> 29
 <212> PRT
 <213> Homo sapiens

<400> 158
 Glu Ser Phe Val Ile Tyr Met Phe Val Val His Phe Thr Ile Pro Met
 1 5 10 15
 Ile Ile Ile Phe Phe Cys Tyr Gly Gln Leu Val Phe Thr
 20 25

<210> 159
 <211> 29
 <212> PRT
 <213> Rattus Norvegicus

<400> 159
 Pro Ile Ile Thr Phe Gly Thr Ala Met Ala Ala Phe Tyr Leu Pro Val
 1 5 10 15

- 131 -

Thr Val Met Cys Thr Leu Tyr Trp Arg Ile Tyr Arg Glu
20 25

<210> 160
<211> 29
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Leu Arg Ile Leu Pro His Thr Phe Gly Phe Ile Val Pro Leu
1 5 10 15

Phe Val Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr
20 25

<210> 161
<211> 29
<212> PRT
<213> Drosophila melanogaster

<400> 161
Arg Gly Tyr Val Ile Tyr Ser Ser Leu Gly Ser Phe Phe Ile Pro Leu
1 5 10 15

Ala Ile Met Thr Ile Val Tyr Ile Glu Ile Phe Val Ala
20 25

<210> 162
<211> 28
<212> PRT
<213> Homo sapiens

<400> 162
Phe Leu Ser Ala Ala Val Phe Cys Ile Phe Ile Ile Cys Phe Gly Pro
1 5 10 15

Thr Asn Val Leu Leu Ile Ala His Tyr Ser Phe Leu
20 25

<210> 163
<211> 28
<212> PRT
<213> Homo sapiens

<400> 163
Arg Met Val Ile Ile Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro
1 5 10 15

Tyr Ala Ser Val Ala Phe Tyr Ile Phe Thr His Gln
20 25

- 132 -

<210> 164
 <211> 28
 <212> PRT
 <213> Rattus Norvegicus

<400> 164
 Arg Thr Leu Ser Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro
 1 5 10 15
 Tyr Asn Ile Met Val Leu Val Ser Thr Phe Cys Lys
 20 25

<210> 165
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 165
 Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro
 1 5 10 15
 Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg
 20 25

<210> 166
 <211> 28
 <212> PRT
 <213> Drosophila melanogaster

<400> 166
 Arg Thr Leu Gly Ile Ile Met Gly Val Phe Val Ile Cys Trp Leu Pro
 1 5 10 15
 Phe Phe Leu Met Tyr Val Ile Leu Pro Phe Cys Gln
 20 25

<210> 167
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 167
 Glu Ala Ala Tyr Phe Ala Tyr Leu Leu Cys Val Cys Val Ser Ser Ile
 1 5 10 15
 Ser Ser Cys Ile Asp Pro Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys
 20 25 30

Gln

<210> 168
 <211> 33
 <212> PRT
 <213> Homo sapiens

- 133 -

<400> 168

Asn Phe Gly Pro Ile Phe Met Thr Ile Pro Ala Phe Phe Ala Lys Ser
1 5 10 15

Ala Ala Ile Tyr Asn Pro Val Ile Tyr Ile Met Met Asn Lys Gln Phe
20 25 30

Arg

<210> 169

<211> 33

<212> PRT

<213> Rattus Norvegicus

<400> 169

Cys Val Pro Glu Thr Leu Trp Glu Leu Gly Tyr Trp Leu Cys Tyr Val
1 5 10 15

Asn Ser Thr Val Asn Pro Met Cys Tyr Ala Leu Cys Asn Lys Ala Phe
20 25 30

Arg

<210> 170

<211> 33

<212> PRT

<213> Homo sapiens

<400> 170

Asn Asn Ile Gly Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu
1 5 10 15

His Ser Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn Phe
20 25 30

Arg

<210> 171

<211> 33

<212> PRT

<213> Drosophila melanogaster

<400> 171

Cys Pro Thr Asn Lys Phe Lys Asn Phe Ile Thr Trp Leu Gly Tyr Ile
1 5 10 15

Asn Ser Gly Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Leu Asp Tyr
20 25 30

Arg

- 134 -

<210> 172
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 7
 transmembrane receptor consensus sequence

<400> 172
 Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
 1 5 10 15
 Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
 20 25 30
 Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln
 35 40 45
 Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
 50 55 60
 Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
 65 70 75 80
 Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
 85 90 95
 Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Trp
 100 105 110
 Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
 115 120 125
 Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile
 130 135 140
 Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr
 145 150 155 160
 Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe
 165 170

<210> 173
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 173
 Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln Lys Lys Trp
 1 5 10 15
 Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr His Met Leu
 20 25 30
 Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln Leu Arg Arg
 35 40 45

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Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys Val Phe Val
50 55 60

Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser Val Thr Ser
65 70 75 80

Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val Asn Tyr Arg
85 90 95

Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met Gly Ile Trp
100 105 110

Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly Trp His Asp
115 120 125

Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile Val Ala Glu
130 135 140

Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val Gly Gly Ser
145 150 155 160

Val Ala Met Gly Val Ile Cys Thr
165

<210> 174

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 174

Ile Gln Glu Arg Met Asn Glu Leu Asn Asp Arg Trp Glu Arg Leu Lys
1 5 10 15

Glu Leu Met Glu Gln Arg Arg Gln Met Leu Glu Asp Ser Met Arg Leu
20 25 30

Gln Gln Phe Phe Arg Asp Met Asp Glu Glu Glu Ser Trp Ile Asn Glu
35 40 45

Lys Glu Gln Ile Leu Asn Ser Asp Asp Tyr Gly Lys Asp Leu Thr Ser
50 55 60

Val Gln Asn Leu Leu Lys Lys His Gln Ala Phe Glu Ala Asp Ile Ala
65 70 75 80

Ala His Glu Asp Arg Ile Gln Ala Leu Asn Glu Phe Ala Gln Gln Leu
85 90 95

Ile Gln Glu Asn His Tyr Ala Ser Glu Glu
100 105

- 136 -

<210> 175
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 175
 Phe Ser Ser Leu Arg Ala Asp Ala Ser Ala Pro Trp Met Ala Leu Cys
 1 5 10 15
 Val Leu Trp Cys Ser Val Ala Gln Ala Leu Leu Leu Pro Val Phe Leu
 20 25 30
 Trp Ala Cys Asp Arg Tyr Arg Ala Asp Leu Lys Ala Val Arg Glu Lys
 35 40 45
 Cys Met Ala Leu Met Ala Asn Asp Glu Glu Ser Asp Asp Glu Thr Ser
 50 55 60
 Leu Glu Gly Gly Ile Ser Pro Asp Leu Val Leu Glu Arg Ser Leu Asp
 65 70 75 80
 Tyr Gly Tyr Gly Gly Asp Phe Val Ala Leu Asp Arg Met Ala Lys Tyr
 85 90 95
 Glu Ile Ser Ala Leu Glu Gly Gly Leu Pro Gln
 100 105

<210> 176
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Xaa at position 2 may be any amino acide except:
 Glu, Asp, Arg, Lys, His, Phe, Pro, Tyr, or Trp

<220>
 <223> Xaa at position 5 may be ser, Thr, Ala, Gly, Cys
 or Asn

<220>
 <223> Xaa at position 6 may be any amino acid except Pro

<220>
 <223> Description of Artificial Sequence: Amidation
 consensus site

<400> 176
 Gly Xaa Xaa Xaa Xaa Xaa
 1 5